

Result No.	Score	Query Match	Length	DB	ID	Description	
1	2323	100.0	417	3	US-08-815-469-4	Sequence 4, Appli	
2	2323	100.0	417	3	US-09-153-927-2	Sequence 2, Appli	
3	2323	100.0	417	3	US-09-565-918-5	Sequence 5, Appli	
4	2323	100.0	417	4	US-08-928-069-10	Sequence 10, Appli	
5	2323	100.0	417	4	US-08-828-683A-6	Sequence 6, Appli	
6	2323	100.0	417	4	US-09-557-908-4	Sequence 4, Appli	
7	2323	100.0	417	4	US-09-874-138-5	Sequence 5, Appli	
8	2323	100.0	417	4	US-09-333-966-4	Sequence 4, Appli	
9	2323	100.0	446	4	US-09-949-016-7652	Sequence 7652, Ap	
10	2323	100.0	833	3	US-09-013-895A-5	Sequence 5, Appli	
11	2323	100.0	833	4	US-09-448-868-5	Sequence 5, Appli	
12	2267	97.6	428	3	US-08-815-469-2	Sequence 2, Appli	
13	2267	97.6	428	4	US-09-557-908-2	Sequence 2, Appli	
14	2267	97.6	428	4	US-09-333-966-2	Sequence 2, Appli	
15	1051	45.2	181	4	US-08-928-069-1	Sequence 1, Appli	
16	1051	45.2	181	4	US-08-828-683A-1	Sequence 1, Appli	
17	387.5	16.7	471	4	US-09-513-007-2	Sequence 1, Appli	
18	376	16.2	455	1	US-08-050-319B-25	Sequence 25, Appli	
19	376	16.2	455	2	US-08-465-982-25	Sequence 25, Appli	
20	376	16.2	455	4	US-08-406-824A-4	Sequence 4, Appli	
21	374.5	16.1	909	3	US-09-013-895A-4	Sequence 4, Appli	
22	374.5	16.1	909	4	US-09-448-868-4	Sequence 4, Appli	
23	374	16.1	455	1	US-08-321-668-2	Sequence 2, Appli	
24	374	16.1	455	1	US-08-837-941-2	Sequence 2, Appli	
25	374	16.1	455	2	US-08-126-016-2	Sequence 2, Appli	
26	374	16.1	455	3	US-08-815-469-5	Sequence 5, Appli	
27	374	16.1	455	3	US-09-006-353A-3	Sequence 3, Appli	

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US-08-815-469-4
Query Match      100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193; Indels 0; Gaps 0;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVBCQVSCVSSSPFFYQPCCLDCGALHRRHRLTLLCSRDDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVBCQVSCVSSSPFFYQPCCLDCGALHRRHRLTLLCSRDDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTAD EAG 240

Qy 241 MEALTPPPATHSLPDSAHITLLAPDSSSEKICTVQLVGNSTWPGYPETQEALCPQVTSW 300
Db 241 MEALTPPPATHSLPDSAHITLLAPDSSSEKICTVQLVGNSTWPGYPETQEALCPQVTSW 300

Qy 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPGPOLYDVMADVAPARRWKEFVRTTGLREAE 360
Db 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPGPOLYDVMADVAPARRWKEFVRTTGLREAE 360

Qy 361 IEAVEVEIGRFDQOQYEMLKWRQOQAPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDQOQYEMLKWRQOQAPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417

RESULT 2
US-09-153-927-2
; Sequence 2, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153.927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061.334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-2

Query Match      100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVBCQVSCVSSSPFFYQPCCLDCGALHRRHRLTLLCSRDDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVBCQVSCVSSSPFFYQPCCLDCGALHRRHRLTLLCSRDDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTAD EAG 240

Qy 241 MEALTPPPATHSLPDSAHITLLAPDSSSEKICTVQLVGNSTWPGYPETQEALCPQVTSW 300
Db 241 MEALTPPPATHSLPDSAHITLLAPDSSSEKICTVQLVGNSTWPGYPETQEALCPQVTSW 300

Qy 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPGPOLYDVMADVAPARRWKEFVRTTGLREAE 360
Db 301 DQPSRALGPAAPTLSPESPAGSPAMMLOPGPOLYDVMADVAPARRWKEFVRTTGLREAE 360

Qy 361 IEAVEVEIGRFDQOQYEMLKWRQOQAPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDQOQYEMLKWRQOQAPAGLGA VAAALERMGLDGCVEDLRSRLQRP 417

US-09-565-918-5
; Sequence 5, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-5

Query Match      100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVBCQVSCVSSSPFFYQPCCLDCGALHRRHRLTLLCSRDDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVBCQVSCVSSSPFFYQPCCLDCGALHRRHRLTLLCSRDDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQFVQVLLAGLVVPLLGLATLTYYRHCWPHKPLVTAD EAG 240

Qy 241 MEALTPPPATHSLPDSAHITLLAPDSSSEKICTVQLVGNSTWPGYPETQEALCPQVTSW 300
Db 241 MEALTPPPATHSLPDSAHITLLAPDSSSEKICTVQLVGNSTWPGYPETQEALCPQVTSW 300
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QY 301 DQPSRALGPAAAPTLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
DB 301 DQPSRALGPAAAPTLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
QY 361 IEAVEVEIGRFDQOQYEMLKRWROOQAGLGAVVAALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGRFDQOQYEMLKRWROOQAGLGAVVAALERMGLDGCVEDLRSRLQGP 417

RESULT 4

US-08-928-069-10
; Sequence 10, Application US/08928069
; Patent No. 6462176
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026943
; FILING DATE: 09/23/1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P105281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-928-069-10

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVEQVQSQVSSSPFYCQPCDCLCGALHRRHRLTLCSRRDTCGTCPLPGFYEHGDCVSCP 180
DB 121 WFVEQVQSQVSSSPFYCQPCDCLCGALHRRHRLTLCSRRDTCGTCPLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCPHPKPLVTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCPHPKPLVTADAG 240
QY 241 MEALTPPPTHLSPLDSAHHTLLAPDSSEKICTVOLVGNWMTPGYPETOEALCPQVTSW 300
DB 241 MEALTPPPTHLSPLDSAHHTLLAPDSSEKICTVOLVGNWMTPGYPETOEALCPQVTSW 300

QY 301 DQPSRALGPAAAPTLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
DB 301 DQPSRALGPAAAPTLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
QY 361 IEAVEVEIGRFDQOQYEMLKRWROOQAGLGAVVAALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGRFDQOQYEMLKRWROOQAGLGAVVAALERMGLDGCVEDLRSRLQGP 417

RESULT 5

US-08-828-683A-6
; Sequence 6, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-828-683A-6

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAVAAALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVEQVQSQVSSSPFYCQPCDCLCGALHRRHRLTLCSRRDTCGTCPLPGFYEHGDCVSCP 180
DB 121 WFVEQVQSQVSSSPFYCQPCDCLCGALHRRHRLTLCSRRDTCGTCPLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCPHPKPLVTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCPHPKPLVTADAG 240

Db 361 IEAVEVEIGRFRDQOYEMLKWRQOQPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 8
US-09-333-966-4
; Sequence 4, Application US/09333966
; Patent No. 6759513
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: 6759513 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-333-966-4

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPGRCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPGRCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG 120

QY 121 WFVEQVQSCVSSSPFYCPCLDCGALHRRHLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
DB 121 WFVEQVQSCVSSSPFYCPCLDCGALHRRHLLCSRRDTCGTCCLPGFYEHGDCVSCP 180

QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADAG 240

QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300
DB 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300

QY 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLLGLRAE 360
DB 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLLGLRAE 360

QY 361 IEAVEVEIGRFRDQOYEMLKWRQOQPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOYEMLKWRQOQPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 9
US-09-949-016-7652
; Sequence 7652, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7652
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7652

Query Match 100.0%; Score 2323; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.2e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPGRCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 30 MEQRPGRCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 89

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG 120
DB 90 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG 149

QY 121 WFVEQVQSCVSSSPFYCPCLDCGALHRRHLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
DB 150 WFVEQVQSCVSSSPFYCPCLDCGALHRRHLLCSRRDTCGTCCLPGFYEHGDCVSCP 209

QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADAG 240
DB 210 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADAG 269

QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300
DB 270 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 329

QY 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLLGLRAE 360
DB 330 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLLGLRAE 389

QY 361 IEAVEVEIGRFRDQOYEMLKWRQOQPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 417
DB 390 IEAVEVEIGRFRDQOYEMLKWRQOQPAGLGAIVAAALERMGLDGCVEDLRSRLQRP 446

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RESULT 10
US-09-013-895A-5
; Sequence 5, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G. L.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013.895A
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-895A-5

Query Match 100.0%; Score 2323; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.7e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVSQCVSSSPFYCQPCDCLGALHRRHLLCSRRDTCGCLPGFYEHGDCVSCP 180
Db 121 WFVECVSQCVSSSPFYCQPCDCLGALHRRHLLCSRRDTCGCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWQMFVQVLLAGLVVPLLGLATLYTVRHCHPPLVTADEAG 240
Db 181 TSTLGSCPERCAAVCGWQMFVQVLLAGLVVPLLGLATLYTVRHCHPPLVTADEAG 240
QY 241 MEALTPTTPTTHLSPLDSSAHTLLAPDSSSEKICTVQLVGNWSTPGYPETQEALCPQVTSW 300
Db 241 MEALTPTTPTTHLSPLDSSAHTLLAPDSSSEKICTVQLVGNWSTPGYPETQEALCPQVTSW 300
QY 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE 360

RESULT 11
US-09-448-868-5
; Sequence 5, Application US/09448868
; Patent No. 6461823
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G. L.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448.868
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-448-868-5

Query Match 100.0%; Score 2323; DB 4; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.7e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVSQCVSSSPFYCQPCDCLGALHRRHLLCSRRDTCGCLPGFYEHGDCVSCP 180
Db 121 WFVECVSQCVSSSPFYCQPCDCLGALHRRHLLCSRRDTCGCLPGFYEHGDCVSCP 180
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QY 181 TSTLSCPERCAACVCGWQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADG 240
DB 181 TSTLSCPERCAACVCGWQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVLVGNSTPGYPETQALCPQVTSW 300
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVLVGNSTPGYPETQALCPQVTSW 300
QY 301 DQPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOYEMLRWQOQPPAGLGAIVAAALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGRFRDQOYEMLRWQOQPPAGLGAIVAAALERMGLDGCVEDLRSRLQGP 417

RESULT 12
US-08-815-469-2
; Sequence 2, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KEM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-815-469-2

Query Match 97.6%; Score 2267; DB 3; Length 428;
Best Local Similarity 97.1%; Pred. No. 8.6e-189;
Matches 409; Conservative 1; Mismatches 5; Indels 6; Gaps 1;

QY 3 QRRPG-----CAVAAALLLVILGARAQGGTRSPRCDGDFHKKIIGLFCRCGCPAGHY 56
DB 8 EAPRGQLRGESAAFPVQALLLVILGARAQGGTRSPRCDGDFHKKIIGLFCRCGCPAGHY 67
QY 57 LKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARCOACDBQASQVALENCASVADTRCG 116
DB 68 LKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARCOACDBQASQVALENCASVADTRCG 127
QY 117 CKPGWFVECVQSQVSSSPFYCQPCLDGALHRRHTRILLCSRRDTCGTCLPGFVEHGDGC 176
DB 128 CKPGWFVECVQSQVSSSPFYCQPCLDGALHRRHTRILLCSRRDTCGTCLPGFVEHGDGC 187
QY 177 VSCPTSTLSCPERCAACVCGWQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTA 236
DB 188 VSCPTSTLSCPERCAACVCGWQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTA 247
QY 237 DEAGMEALTPPPATHLSPLDSAHLLAPPDSSEKICTVLVGNSTPGYPETQALCPQV 296
DB 248 DEAGMEALTPPPATHLSPLDSAHLLAPPDSSEKICTVLVGNSTPGYPETQALCPQV 307
QY 297 TWSMDQLPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGL 356
DB 308 TWSMDQLPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGL 367
QY 357 REAEIEAVEVEIGRFRDQOYEMLRWQOQPPAGLGAIVAAALERMGLDGCVEDLRSRLQGP 416
DB 368 REAEIEAVEVEIGRFRDQOYEMLRWQOQPPAGLGAIVAAALERMGLDGCVEDLRSRLQGP 427
QY 417 P 417
DB 428 P 428

RESULT 13
US-09-557-908-2
; Sequence 2, Application US/09557908
; Patent No. 6713061
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; FILE REFERENCE: 1488.0310008
; CURRENT APPLICATION NUMBER: US/09/557,908
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 60/136,741
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/130,488
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 08/815,469
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: US 60/037,341
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/028,711
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/013,285
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-908-2

Query Match 97.6%; Score 2267; DB 4; Length 428;
Best Local Similarity 97.1%; Pred. No. 8.6e-189;
Matches 409; Conservative 1; Mismatches 5; Indels 6; Gaps 1;
QY 3 QRRPG-----CAVAAALLLVILGARAQGGTRSPRCDGDFHKKIIGLFCRCGCPAGHY 56


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;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026943
; FILING DATE: 09/23/1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-928-069-1

Query Match 45.2%; Score 1051; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.3e-83;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120

Qy 121 WFVECVQSVQCVSSSPFYCQPCLDGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSVQCVSSSPFYCQPCLDGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180

Qy 181 T 181
Db 181 T 181
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Search completed: June 27, 2005, 13:44:23
Job time : 46 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:37:13 ; Search time 19 Seconds
(without alignments)

2111.705 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAVAAALLLVLL.....ERMGLDGCVEDLRSLQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415	17.9	461	2 JC4302	tumor necrosis fac
2	404.5	17.4	454	1 GOMST1	tumor necrosis fac
3	394.5	17.0	461	1 GORTT1	tumor necrosis fac
4	374	16.1	455	1 GORTU1	tumor necrosis fac
5	199.5	8.6	335	2 A40036	apoptosis-mediati
6	196	8.4	327	2 A46484	apoptosis-mediati
7	175	7.5	324	2 JC2395	Fas antigen precu
8	168	7.2	314	2 I37383	FAS soluble protei
9	166	7.1	435	2 I54182	tumor necrosis fac
10	163.5	7.0	1548	2 S34583	serine proteinase
11	162.5	7.0	349	2 D36858	gene G4R protein -
12	159.5	6.9	348	2 T28623	hypothetical prote
13	158	6.8	425	1 A26431	nerve growth facto
14	158	6.8	1574	2 T13954	MEGF6 protein - ra
15	155.5	6.7	427	1 GQHUN	nerve growth facto
16	154.5	6.7	349	2 D72175	G2R protein - vari
17	153.5	6.6	272	2 I48700	gene ox40 protein
18	153.5	6.6	651	2 JC7705	death receptor-6 -
19	153.5	6.6	915	1 A48225	subtilisin-like pr
20	149.5	6.4	3707	2 S18252	heparan sulfate pr
21	148	6.4	2823	2 F87908	protein T22A3.8 li
22	148	6.4	2823	2 T23064	hypothetical prote
23	148	6.4	3102	2 T43291	laminin alpha chai
24	147.5	6.3	1801	1 MMRTS	laminin beta-2 cha
25	146.5	6.3	2531	2 T31070	notch homolog - se
26	146	6.3	277	2 A60771	B-cell activation
27	146	6.3	667	2 A48579	trophozoite surfac
28	145.5	6.3	416	1 JN0006	nerve growth facto
29	145	6.2	3635	2 T10053	laminin alpha 5 ch

30	144.5	6.2	326	1 GQVZML	T2 protein - myxom
31	144.5	6.2	1680	2 A43434	furin (EC 3.4.21.7
32	143.5	6.2	915	2 B48225	probable proteol
33	143.5	6.2	4391	2 A38096	perlecan precursor
34	142	6.1	1557	2 T28811	hypothetical prote
35	141.5	6.1	686	2 JC7569	Delta-4 protein -
36	138.5	6.0	1299	2 T43251	furin (EC 3.4.21.7
37	138	5.9	271	2 S12783	OX40 antigen precu
38	138	5.9	305	2 A46476	B cell-associated
39	138	5.9	1607	1 MMMSB2	laminin gamma-1 ch
40	138	5.9	1609	1 MMHUB2	laminin gamma-1 ch
41	137.5	5.9	642	1 S52111	uromodulin precurs
42	137.5	5.9	1798	2 S53869	laminin beta-2 cha
43	136.5	5.9	260	1 A46517	CD27 antigen precu
44	136.5	5.9	2219	2 T27684	hypothetical prote
45	136.5	5.9	3712	2 S18253	laminin alpha-1 ch

ALIGNMENTS

RESULT 1

JC4302

tumor necrosis factor receptor p55 precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C:Accession: JC4302; PC4093

R:Suter, B.; Pauli, U.

Gene 163, 263-266, 1995

A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A:Reference number: JC4302; MUID:96011645; PMID:7590278

A:Accession: JC4302

A:Molecule type: mRNA

A:Residues: 1-461 <SUT>

A:Cross-references: UNIPROT:P50555; GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g114175

A:Accession: PC4093

A:Molecule type: protein

A:Residues: 1-7 <SU2>

A:Experimental source: kidney cell line 15

C:Genetics:

A:Gene: tnfr

C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>

F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NGF>

F:211-231/Domain: transmembrane #status predicted <TMM>

F:361-447/Domain: signal transduction #status predicted <SIT>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.9%; Score 415; DB 2; Length 461;

Best Local Similarity 30.5%; Pred. No. 1.5e-20;

Matches 140; Conservative 44; Mismatches 201; Indels 74; Gaps 18;

QY 11 VAAALLVLLGARAQG-----GTRSPR---CDCAGDFHKIGLFCRCGCPAGHYLKAPCT 62

Db 14 VLRAALLVDVYPAGVGLVHFGDREKRESLCPQGYKSHPNRSICCTCKHGKGYLLHNDCL 73

QY 63 BPCGNSTCLVCPQDTFLAWHNHNSCARQACDEQASQVALENSAVADTRCGCKPGWF 122

Db 74 GPGLDTDCRECDNGTFTASEN-HLTQCLSCSKRSEMSQVSEISPTVDRTDTCVCGCRKN-- 130

QY 123 VECQVSQCVSSSPFCQPCLDGALHRRHTRLLC-SRRDTCGTCLPGFYEHGDCGVCSPCT 181

Db 131 ---QTRKTSWSTLFOCLNCSLCP--NGTVQLPCLKQDTIC-NCHSGFFLDKECVSCVN 184

QY 182 STLGSCPCERCAAVCGWRQMF-----WVQVLLAGLVVPLLLGATLTFTYTHCWPH--- 230

Db 185 CKNADCKNLCPATSETRNDFTGTGTVLLPLVIFPGLCLAFFLVGLACRYQWRKPKLYS 244

QY 231 -----KPLVTADGAGMEALTPPPATHLSPLD--SAHTLLAPDSSSEKICTV 274

Db 245 IICGKSTPVKEGEPEPLATAPSG-----PIITFSPISPSPTTTPSPVPSFPISSP 297
QY 275 QLVGNSWT---PGVPETQEQALCPQVTSWDQLPSRALGPAAPATLSP-----ESPAG 323
Db 298 TFTPDCWNSNIKVTGPKKEIAPPQAG-----PILMPAPPASTPPTPLPKWGGSAHSAHS 352
QY 324 SPAMMLQGP-QLYDMDAVPARWKFEVRTLGLREAEIEAVEVEIGR-FRDQOQVEMLKR 381
Db 353 APAQLADADPATLYAVDGVPTTRWKFEVRRRLGLSEHIELELQNGCLREAOYSLMAE 412
QY 382 WRQ-----QQPAGLGVYAALERMGLDGCVEDLSRLQRP 417
Db 413 WRRRTSRREATLELLGSLVRDMDLLGLCLEDIEAL-RGP 450
RESULT 2
QOMST1
N: tumor necrosis factor receptor 1 precursor - mouse
C: Species: Mus musculus (house mouse)
C: Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
C: Accession: A38634; B40254; S16677; S19021; I54532; I57826
R: Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A: Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A: Reference number: A38634; MUID: 91187885; PMID: 1849278
A: Accession: A38634
A: Molecule type: mRNA
A: Residues: 1-454 <LEW>
A: Cross-references: UNIPROT: P25118; GB: M60468; NID: g199825; PIDN: AAA39751.1; PID: g199826
R: Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A: Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A: Reference number: A40254; MUID: 91246168; PMID: 1645445
A: Accession: B40254
A: Molecule type: mRNA
A: Residues: 1-454 <GO>
A: Cross-references: GB: M60468; NID: g199825; PIDN: AAA39751.1; PID: g199826
R: Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldma
Eur. J. Immunol. 21, 1649-1656, 1991
A: Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
A: Reference number: S16677; MUID: 91285014; PMID: 1647956
A: Accession: S16677
A: Molecule type: mRNA
A: Residues: 1-454 <BAR>
A: Cross-references: EMBL: X59238; NID: G53578; PIDN: CAA41922.1; PID: G53579
R: Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A: Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A: Reference number: S19021; MUID: 92039815; PMID: 1657766
A: Accession: S19021
A: Molecule type: mRNA
A: Residues: 1-454 <ROT>
A: Cross-references: EMBL: X57796; NID: G54848; PIDN: CAA40936.1; PID: G54849
R: Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A: Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1
A: Reference number: I54532; MUID: 94245292; PMID: 8188324
A: Accession: I54532
A: Status: translated from GB/EMBL/DBDJ
A: Molecule type: mRNA
A: Residues: 1-454 <RES>
A: Cross-references: GB: L26349; NID: g430732; PIDN: AAA59361.1; PID: g430733
R: Rothe, J.G.; Bluthmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A: Title: Genomic organization and promoter function of the murine tumor necrosis factor
A: Reference number: I57826; MUID: 93156721; PMID: 8381516
A: Accession: I57826
A: Status: preliminary; translated from GB/EMBL/DBDJ
A: Molecule type: DNA
A: Residues: 1-393, 'G', 395-454 <RE2>
A: Cross-references: GB: M76656; NID: g202100; PIDN: AAA40465.1; PID: g202102

C: Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C: Genetics:
A: Gene: TNFR-2
A: Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C: Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C: Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein
F: 1-29/Domain: signal sequence #status predicted <SIG>
F: 30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F: 30-212/Domain: extracellular #status predicted <EXT>
F: 44-82/Domain: NGF receptor repeat homology <NG1>
F: 84-126/Domain: NGF receptor repeat homology <NG2>
F: 127-167/Domain: NGF receptor repeat homology <NG3>
F: 168-204/Domain: NGF receptor repeat homology <NG4>
F: 213-235/Domain: transmembrane #status predicted <MEM>
F: 236-454/Domain: intracellular #status predicted <INT>
F: 54,151,202/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 17.4%; Score 404.5; DB 1; Length 454;
Best Local Similarity 27.2%; Pred. No. 7.5e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;
QY 11 VAAALLIVILGARQGGT-----RSPRCDCAGDPHKKILGLFCCRCPCPAGHYLKA 59
DB 11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDLSLCPQGYVHSKNNSICCTCKCHKGTLYVS 70
QY 60 PCTEPCGNSTCLVCPDPTFLAWENHNHNSCARCOACDEOASQVALENCASAVADTRCGCKP 119
DB 71 DCSPGRDTCRECEKGTFTTASQNYLR-QCLSCYCKEMSOVEISPCQADKDTVCCK- 128
QY 120 GWFVECVQSVSSPPYCYQCLDCGALHRRHLLCSRRTDCTCLPGFVEHGDGCVSC 179
DB 129 ----ENQFQVLSBTHFQVDCSPC--FNGVTVPCKETQNTVCNCHAGFFLRESECVPC 182
QY 180 PTSTLGSCLP--ERCAAVC-----GWQMFVQVVLGLVPLLLGATLTY 224
DB 183 ----SHCKXNEECMKGLCPPLANVTPQDSGPAVLPLVLLGLCLLSFIFSLMCRY 237
QY 225 RHQWP-----HKPLVTADGMEALTPPPATHLSPLDSAHTLL-----APDSEK 270
DB 238 PRWRPEVYSIICRDPVPVKEKAGKPLTPAPSPAFSTSGFNPLTGSTPGFSSPVSTP 297
QY 271 ICTVOLVGNW-----FTGY-PETQEQALC----POVTVSWDQLPSRALGPAAP 314
DB 298 ISPI-FGFSNWHFPPVSEVVPTQADPLLYESLCSVPAPTSVQKWD----- 344
QY 315 TLPSPAGSPAMMLQPGPOLYDMDAVPARRWKFEVRTLGLREAEIEAVEVEIGR-FRD 373
DB 345 SAHPQRPDNADLAI-----LYAVDGVPPARWKFEVRRRLGLSEHIELELMQNGRCLURE 398
QY 374 QQYEMLKRWRQQQPA---GLGAVVAALERMGLDGCVEDLSRLQRP 417
DB 399 AQYSMLEAWRRRTPRHEDTLEVVGLVLSKNLACLENILEAL-RNP 444
RESULT 3
QORTT1
N: tumor necrosis factor receptor 1 precursor - rat
C: Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C: Species: Rattus norvegicus (Norway rat)
C: Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C: Accession: B36555
R: Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C
DNA Cell Biol. 9, 705-715, 1990
A: Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
A: Reference number: A36555; MUID: 91090841; PMID: 1702293
A: Accession: B36555
A: Molecule type: mRNA
A: Residues: 1-461 <HIM>
A: Cross-references: UNIPROT: P22934; GB: M63122; NID: g207361; PIDN: AAA42256.1; PID: g207362
C: Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C: Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C: Keywords: duplication; glycoprotein; receptor; transmembrane protein
F: 1-29/Domain: signal sequence #status predicted <SIG>

A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
F:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: JC2404; MUID:95128033; PMID:7765720
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53, 'X', '55-144, 'X', '146-150, 'X', '152-186, 'X', '188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <INT>
F:235-455/Domain: intracellular #status predicted <MEM>
F:54, 145, 151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.1%; Score 374; DB 1; Length 455;
Best Local Similarity 28.3%; Pred. No. 8.2e-18;
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;

Qy 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
Db 15 LLELVGLYPSGVGLVPHLGDRKRSVCPQGYKIHPPNNISICTCKHGTLYINDCPG 74

Qy 64 PCGNSTCLVCPQDTFLAWENHNHSECARCQACDQASQVALENGSADVATRCGCKPGWFFV 123
Db 75 PGQDTDCRECSGSFTASENHLR-HCLSCSKCKEMGQVEISSCTVDRDITVCGCRKNQYR 133

Qy 124 EC---QVSQCVSSSPFFYQPCDCLDGHRLHRLTLCSRRDTCGCLPGFYEHGDCVSCVP 180
Db 134 HYWSENLFQC-----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 182

Qy 181 TSTLGSCPE--RCAAVC-----GWRQMFVQVLLAGLVVPLLLGATILTYTYRH 226
Db 183 ----SNCKSLSECTKCLPQENVKGTEDSGTTLVLLPLVIFGLLSLLFGLMYRYQR 238

Qy 227 CWPHK-----PLVTADAEAGMEALTPPPATHPLSPLDS-----AHTLAPDPSSEKIC 272
Db 239 -WKSPLYIVCGKSTPEKEGELEGTTPK---LAPNFSFPTPGFTPLGLSPVPSSTFT 294

Qy 273 TVQLVGNWTPGYPETQALCPQVTSWDQLPSRALGP-----AAAPTJLSP- 318
Db 295 S-----STYTPFGD-----CPNFA-----APREVAPPYQAGDPIALALASDPIPNPL 338

Qy 319 ---ESPAGSPAMMLQPGP-QLYDVMDVAVPARRWKEFVTLGLREAEIETAVEVEIGR-FRD 373
Db 339 QKWDSAHKPOSLODDPATLYAVVENVPLRWKEFVRLGLSDHEIDRLQLQNGRCURE 398

Qy 374 QQYEMLKRWQQQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
Db 399 AQYSMLATWRRRTPRREATLELLGRVLRMDMLLGLCLEDIEAL 441

RESULT 5
A40036

apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A40036; S24543; A38142
R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, H.
Cell 66, 233-243, 1991
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediat
A:Reference number: A40036; MUID:91309137; PMID:1713127
A:Accession: A40036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <ITO>
A:Cross-references: UNIPROT:P25445; GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
R:Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A:Reference number: S24543
A:Accession: S24543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <KRA>
A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Richter
J. Biol. Chem. 267, 10709-10715, 1992
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member c
A:Reference number: A38142; MUID:92268122; PMID:1375228
A:Accession: A38142
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-134, 'Q', '136-335 <OEH>
A:Experimental source: SKW6.4 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)
A:Note: in NCBI backbone the source is designated as mouse
C:Genetics:
A:Gene: GDB:APTL
A:Cross-references: GDB:132671; OMIM:134637
A:Map position: 10q24.1-10q24.1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: apoptosis; surface antigen; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:85-128/Domain: NGF receptor repeat homology <NG4>
F:174-190/Domain: transmembrane #status predicted <TMM>

Query Match 8.6%; Score 199.5; DB 2; Length 335;
Best Local Similarity 21.4%; Pred. No. 2.8e-06;
Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;

Qy 44 GLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQASQVA 103
Db 56 GQFCHKPCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRRCLCDEGHGLEV 115

Qy 104 LENCASADVATRCGCKPGWFFVEQVSCVSSSPFFYQPCDCLDGHRLHRLTLCSRRDTCG 163
Db 116 EINCRTQNTKCRCKNFF-----CNSTVCEHCDPCTKC----- 149

Qy 164 TCLPGFYEHGDCGVCSTLGLSCPCERCAAVCGWR-QMFVQVLLAGLVVPLLLGATILTY 222
Db 150 -----EHGI-IKECTLTSTNCKEE-----GSRNLGWLCLLL--LPITLIWVRKE 194

Qy 223 TYRHCWPHKPLVTADAEAGMEALTPPPATHPLSPLDSAHTL---LAPDPSSEKICTVQLVGN 279
Db 195 VQKTCRKHRR---KENQG-----SHESPTLNPTVAINTLSDVLSKYITTI----- 236

Qy 280 SWTPGYETQALCPQVTSWDQLPSRALGFAAPTILSPSPAGSPAMMLQPGQLVDVM 339
Db 237 -----AGVTLS----- 243

Qy 340 DAVPARRWKEFVTLGLREAEIETAVEVE-IGRFRDQQYEMLKRWQ 384
Db 244 -----QVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNWHQ 283

RESULT 6

A46484
apoptosis-mediating membrane-associated polypeptide Fas - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J. Immunol. 148, 1274-1279, 1992
A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas and Fas ligand genes
A:Reference number: A46484; MUID:92148151; PMID:1371136
A:Accession: A46484
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-327 <WAT>
A:Cross-references: UNIPROT:P25446; GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A:Experimental source: BAW3 macrophage cell line
A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A:Title: Aberrant transcription caused by the insertion of an early transposable element
A:Reference number: A47254; MUID:93189576; PMID:7680478
A:Accession: A47254
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <ADA>
A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A:Experimental source: MRL lpr/lpr
A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863, NCBIN:126864)
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: transmembrane protein
F:44-79/Domain: NGF receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 8.4%; Score 196; DB 2; Length 327;
Best Local Similarity 23.8%; Pred. No. 4.7e-06;
Matches 62; Conservative 25; Mismatches 109; Indels 64; Gaps 8;

Qy 13 AALLVLGARAQGGTRSPRC-----DCAGDFHKKIGLFCRCGCPAGHY 56
Db 6 AVLPLVLGSQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQG-GPFCQCPQPKK 64
Qy 57 LKAPCTPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENSAVADTRCG 116
Db 65 KVEDCKWNGGTPCAPCTEGKEYMDKNHYDKRCRTCLCDEHGLEVEVETNCTLTQNTCK 124
Qy 117 CKPGHVEFCQVSCVSSSFFYQCPCLDCGALHRRHRLLCSSRRDTCGCLPGFVEHGDGC 176
Db 125 CKP-----DFYCDSE-----FG-CEHCVRVC 142
Qy 177 VSCPTSTLGCSPERCAAVC---GWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPL 233
Db 143 ASCEHGTLEPCTATNTNCRKQSPNRLWLLTLV-LLIPLVF-IYRKYRKRCWKRRQD 200
Qy 234 VTADAGMEALTPPPATHLS 253
Db 201 DPESRTSSRETIPTMASNLS 220

RESULT 7
JC2395
Fas antigen precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: JC2395; PC2246
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A:Reference number: JC2395; MUID:94128114; PMID:7507668
A:Accession: JC2395
A:Molecule type: mRNA
A:Residues: 1-324 <KIM>
A:Cross-references: UNIPROT:Q63199; DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:dl005
A:Experimental source: thymus
A:Accession: PC2246

A:Molecule type: mRNA
A:Residues: 1-62, 'RFT' <XI2>
A:Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:dl005651; PID:g468489
A:Experimental source: liver
C:Genetics:
A:Introns: 62/1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-324/Product: Fas antigen #status predicted <MAT>
F:44-79/Domain: NGF receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NG4>
F:171-188/Domain: transmembrane #status predicted <TMM>

Query Match 7.5%; Score 175; DB 2; Length 324;
Best Local Similarity 28.5%; Pred. No. 0.00012;
Matches 43; Conservative 17; Mismatches 67; Indels 24; Gaps 5;

Qy 11 VARALLVLVG---ARAQG-----GTRSPRCDCAGDFHKKIGLFCRCGCPAG 54
Db 4 IMAVLPLVLGAPFELNVRMQGTDSTFEGLELKRVRVETDNNCSGLY-QVGPFCCQCPQG 62
Qy 55 HYLKAPCTPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENSAVADTR 114
Db 63 ERKYKDCITTSAGPTCHPCTEGEYTDKHYSDKRCRCAFCDEGHGLEVEVETNCTLTQNTK 122
Qy 115 CGCKPGHVEFCQVSCVSSSFFYQCPCLDCG 145
Db 123 CRCKENFY--CNASLIC-----DHCYHCTSCG 146

RESULT 8
I37383
FAS soluble protein - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I37383
R:Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are
A:Reference number: I37383; MUID:95181785; PMID:7533181
A:Accession: I37383
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <RES>
A:Cross-references: UNIPROT:P25445; EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g69555
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

Query Match 7.2%; Score 168; DB 2; Length 314;
Best Local Similarity 19.1%; Pred. No. 0.00034;
Matches 66; Conservative 37; Mismatches 100; Indels 142; Gaps 10;

Qy 44 GLFCRCGPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVA 103
Db 56 GQFCHKPCPGERKARDCTVNGDEPDVPCQEGEYTDKAHFSKRCRCLCDEGHGLEV 115
Qy 104 LENSASVADTRCGCKPGHVEFCQVSCVSSSFFYQCPCLDCGALHRRHRLLCSSRRDTCG 163
Db 116 EINCTRTQNTKRCRKNPF-----CNSTVCEHCDPCTKC----- 149
Qy 164 TCLPGFVEHGDGCVCPTSTLGCSPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLT 223
Db 150 -----EHGI-IKECTLTNTCKEE-----VVRKEV 174
Qy 224 YRHCHPHKPLVTADAGMEALTPPPATHLSPLDSAHTL---LAPDSSEKICTVOLVGN 280
Db 175 QKTCRKR-----KENQG-----SHESFLPVPETVAINLSVDLSKYITTI----- 215
Qy 281 WTPGYPETEALCPQVTSWDQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYVMD 340
Db 216 -----AGVMTLS----- 222
Qy 341 AVPARRWKEFVRTILGLREAEVEVE-IGFRDQOQYEMLKRWQ 384


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Query Match          7.0%; Score 162.5; DB 2; Length 349;
Best Local Similarity 26.7%; Pred. No. 0.00087;
Matches 48; Conservative 21; Mismatches 84; Indels 27; Gaps 10;

Qy 15 LLLVLLGARAQGTRSPRCDGADPHKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCP 74
Db 12 LSCIIINGRDAAPYTPNGKCKDTEYKRNHLCCLSCPPGYASRLCDSKT-NTQCTPCG 69

Qy 75 QDTFLAWENHNHNSCARCOA-CDEQASQVALENCNSAVADTRCGCKPGFWFVECVSQSVSS 133
Db 70 SGTFTS-RNNHLPACLSNCRGN--SNQVETRSCNTHNRICECSPGYY-----CLLK 119

Qy 134 SPFYCQPCLD---CG---ALHRHTLLCSRDTDCGTCLPGFYEY-----GDGCVSCPTST 183
Db 120 GSSGCKACVSQTKGIGYGVSGHT----SVGDVICSPCGFGTYSHTVSSADKCEPVPNNT 175

RESULT 12
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28623
R;Masung, R.F.; Eposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: UNIPROT:P34015; EMBL:L22579; NID:G623595; PIDN:AAA60933.1; PID:G4391
A;Experimental source: strain Bangladesh 1975
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match          6.9%; Score 159.5; DB 2; Length 348;
Best Local Similarity 26.8%; Pred. No. 0.0014;
Matches 48; Conservative 20; Mismatches 84; Indels 27; Gaps 10;

Qy 16 LLLVLLGARAQGTRSPRCDGADPHKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQ 75
Db 12 LSCIIINGRDAAPYTPNGKCKDTEYKRNHLCCLSCPPGYASRLCDSKT-NTQCTPCGS 69

Qy 76 DTFLEWENHNHNSCARCOA-CDEQASQVALENCNSAVADTRCGCKPGFWFVECVSQSVSS 134
Db 70 GTFTS-RNNHLPACLSNCRGN--SNQVETRSCNTHNRICECSPGYY-----CLLK 119

Qy 135 PFYCQPCLD---CG---ALHRHTLLCSRDTDCGTCLPGFYEY-----GDGCVSCPTST 183
Db 120 SSGCKACVSQTKGIGYGVSGHT----SVGDVICSPCGFGTYSHTVSSADKCEPVPNNT 174

RESULT 13
A26431
nerve growth factor receptor precursor, low affinity - rat
N;Alternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A;Reference number: A26431; MUID:87115859; PMID:3027580
A;Accession: A26431
A;Molecule type: mRNA
A;Residues: 1-425 <RAD>
A;Cross-references: UNIPROT:P07174; GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756
R;Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A;Title: Regulatory elements and transcriptional regulation by testosterone and retinoid
A;Reference number: PH1229; MUID:93077038; PMID:1446821
A;Accession: PH1229
A;Molecule type: DNA
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A;Residues: 1-20 <MET>
A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-425/Product: nerve growth factor receptor #status predicted <MAY>
F;30-253/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NGL>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
F;150-190/Domain: NGF receptor repeat homology <NG4>
F;198-249/Region: serine/threonine-rich
F;252-273/Domain: transmembrane #status predicted <MEM>
F;274-425/Domain: intracellular #status predicted <INT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          6.8%; Score 158; DB 1; Length 425;
Best Local Similarity 21.2%; Pred. No. 0.0021;
Matches 102; Conservative 42; Mismatches 202; Indels 136; Gaps 21;

Qy 1 MEQPRGCAAV--AAALLVLLGARAQGTSPRCDGADPHKIGLFCRCGCPAGHYLK 58
Db 1 MRRAGAACSAMDRLRLLLLLILGV--SSGAKG---TCSTGLYTHSG--ECCKACNLGEGVA 55

Qy 59 APC-----TEPCGNSCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASVAD 112
Db 56 QPCGANQTVCEPCLDN---VTFSDVVSATE-----PCKPCTECIGLQMSA--PCVEADD 105

Qy 113 TRCCKPGWFE-----CQVSQCVSSSPFYCQPCLDCCGALHRLHLLCSRRDTCGT 164
Db 106 AVCRCAYGYQDESTGHCEACSVCEVSGLVFSCQ-----DKQNTVCEE 149

Qy 165 CLPGFY----EHGDCGVCSCPT-----STLGSCEPCRAVCGWRQMFVQVLLAGLVVPLL 215
Db 150 CPEGTYSDEANHVDPCLPCTVCEDETRQLRECTPWADACEEIPGRWI----- 197

Qy 216 LGATLTYRHCHWPKPLVTADEAGMEALTP-----PPATHSLPDSLAHTLLAPPSS 268
Db 198 -----PRSTPE--GSDSTABSTOEPEVPEPQDLVPSTVADMTVTVMGSS 240

Qy 269 EKICTVLQVGNWTPGYPETOEA---LCPQVTVS--WDQLPSRALGPAAPTLSPESPAG 323
Db 241 QPVVTRGTTDN-LIPVYCSILAAVVVGLVAVIAFKWNKSKQKQKQNSRPNQTPPEEG 299

Qy 324 -----SPAMMIQPGFQLY-----DVMDAVPARRWKE 349
Db 300 EKLHSDSGISVDSQSLHDQQTHTQTASQALKGDGNYLSPLTKREEVEKLLNGDTWRH 359

Qy 350 FVRTLGLREABIEAVEVEIGFRDQOYEMLEKRWQQQAGLGAVYAAALERMGLDGCVEDL 409
Db 360 LAGELGYQPEHIDSFTHACVPR-----ALLASWGAQDSATLDALLAURLRIQRADIVESL 415

Qy 410 RS 411
Db 416 CS 417

RESULT 14
T13954
MEGF6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13954
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A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:93449293; PIDN:BAA32462.1; PID:93449293
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 6.8%; Score 158; DB 2; Length 1574;
Best Local Similarity 24.5%; Pred. No. 0.0072;
Matches 90; Conservative 16; Mismatches 120; Indels 142; Gaps 23;

Qy 30 SPRCDACGDFHKKIGLFCRCPCAGHY-----LKPCTEPCGNS*CLV----- 72
Db 933 SGACTCPAGWR--GSFCEHACPAAGFFGLDCDSACNSAGAPCDVAVTGSCICPAGRWGPR 989

Qy 73 ----CPQDTFLAWENHNSECARQACDEQASQVALENCNSAVADTRCCKPGWF----- 122
Db 990 CAQSCFPLTF-----GLNCSQICTCFNGAS-----CDSVTG-QCHCAPGMWGPTCLQ 1035

Qy 123 -----VEQVSOVCVSSSPFYCOPCL-DCGALHRRHRLLCSSRDTCGTCLEGFYE-- 171
Db 1036 ACPGLYGNQNS-CLCRNGRCRDPILGQCTCEGWTGLACENE-----CLPGHYAAG 1088

Qy 172 -----HGDGC-----VSCPTSTLG-SCPERRCA-----AVC----- 195
Db 1089 COLNCSCLHGGICDRLTGCHCLCPAGWTGDKCQSSCVSGTFGVHCEHCACRKGASCHHVT 1148

Qy 196 -----GWRQFWVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADEAGMALTPPP 248
Db 1149 GACFCPPGWRGPHCEQAQCFRWFGEACARQLCPTNASC--HH--VTG-----ECRCPPG 1199

Qy 249 ATHLSPLDSANTHLLAPPDSSEKICTVQLVGNWSWTPG-YPETQEAL--CPQVTSWDQLPS 305
Db 1200 FTGL-----SCEQAC-----QPGTFGKDCHELCQCPGETWACD--PA 1234

Qy 306 RALGPFAA 313
Db 1235 SGVCTCAA 1242

RESULT 15
GQHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C:Accession: A25218; A60204; S21689; I57638
R:Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218; MUID:87051725; PMID:3022937
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <JOH>
A:Cross-references: UNIPROT:P08138; GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205
R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.; J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A:Reference number: A60204; MUID:87085574; PMID:3025363
A:Accession: A60204
A:Molecule type: protein
A:Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A:Experimental source: melanoma cell line A875
R:Visavajjalata, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor
A:Reference number: S21689; MUID:92198017; PMID:1372492
A:Accession: S21689
A>Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>

R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor (NGF-R) in a variety of cell types.
A:Reference number: I57638; MUID:89096903; PMID:2850481
A:Accession: I57638
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells, and on a variety of other cell types. The cytosolic domain may form part or all of a complex with the extracellular domain. This protein is thought to form a high-affinity receptor when it associates with the extracellular domain. This receptor undergoes both N- and O-linked glycosylation.
C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:I20234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; tyrosine kinase; signal sequence #status predicted <SIG>
F:1-28/Domain: signal sequence #status predicted <EXT>
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
F:29-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>
F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TRM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.7%; Score 155.5; DB 1; Length 427;
Best Local Similarity 22.1%; Pred. No. 0.0031;
Matches 104; Conservative 36; Mismatches 191; Indels 139; Gaps 21;

Qy 15 LLLVLLGAGGQGTSPRCDCAGDFHKKIGLFCRCPCAGHYKAPC-----TEPCGNS 68
Db 16 LLLLLLGV-SLGGAKEA--CPTGLYTHSG-ECKACNLGEGVAQPCGANQTVCEPCLD 70

Qy 69 TCVCPQDTFLAWENHNSECARQACDEQASQVALENCNSA----VADTRCGCKPGWFVE 124
Db 71 ---VTFSDVVSATE-----PCKPCTEC-----VGLQMSAPCVAEADDAVCRCAAYGYQD 116

Qy 125 -----COVSQCVSSSPFYCOPCLDCGALHRRHRLLCSSRDTCGTCLEGFY-----EH 172
Db 117 ETTGRCACRCVCEAGSLGVFSQ-----DKQNTVCECPDGTYSDEANH 160

Qy 173 GDGCVSCPT-----STLGSCPERCAAVCGWRQFWVQVLLAGLVVPLLLGATLTYYRHC 227
Db 161 VDPCLPCTVCEDTERQLRECTRWADACEBI PGRWIT----- 197

Qy 228 WPHKPLVTADEAGMEALTP--PPATHSLPDSANTHLLAPPDSSEKICTVQLVGNWSWTPGY 285
Db 198 -RSTPPEGSDSTAPSTQEPPEAQEDLIASVAGVVTVMGSSQPVVTRGTTDN-LIPVY 255

Qy 286 PETQEAL-----CPQVTSWDQLPSRALGPFAAAPTLLSPESPAGSPAMML- 329
Db 256 CSILAAVVVGLVAVIAPKRWNSKQNGANSRPNQTPPEGEKLSHDSGISVDSQSLH 315

Qy 330 --QPGPQ-----LYDVMADVAPRR-----WKFEFVRTLGLREAEI 361
Db 316 DQPHPTQTASGQALKGDGGLYSSLP--PAKREEVEKLINGSAGDTWRHLAGELGYQPEHI 373

Qy 362 EAVEVEIGRFRDQOYEMKRWQOQAPAGLCAVVAALERMGLDGCVEILRS 411
Db 374 DSFTHACPVPR-----ALLASWATQDSATLDALLAALRRIQRADLVESLCS 419

Search completed: June 27, 2005, 13:40:44
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:37:13 ; Search time 176 Seconds
(without alignments)
1213.279 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAVAAALLLVLL.....ERMGLDGCVEDLRSLRQGP 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2323	100.0	417	1	TR25_HUMAN	Q93038 h tumor nec
2	1397	60.1	413	2	Q99MM1	Q99mm1 mus musculus
3	1255	54.0	387	2	Q8VD70	Q8vd70 mus musculus
4	415	17.9	461	1	TR1A_PIG	P50555 sus scrofa
5	406.5	17.5	440	2	Q6QHFO	Q6qhfo mus musculus
6	405.5	17.5	440	2	Q6QHF2	Q6qhf2 mus musculus
7	404.5	17.4	440	2	Q6QHFI	Q6qhfi mus musculus
8	404.5	17.4	454	1	TR1A_MOUSE	P25118 mus musculus
9	394.5	17.0	461	1	TR1A_RAT	P22934 rattus norv
10	387.5	16.7	471	1	TR1A_BOVIN	O19131 bos taurus
11	374	16.1	455	1	TR1A_HUMAN	P19438 homo sapien
12	365	15.7	446	2	Q95ND3	Q95nd3 felis silve
13	247.5	10.7	332	1	TRN6_PIG	O77736 sus scrofa
14	226	9.7	319	2	Q9TV79	Q9tcv79 oryctolagus
15	223.5	9.6	389	2	Q6NUU6	Q6nuu6 brachydanio
16	221	9.5	314	2	Q861W6	Q861w6 felis silve
17	217.5	9.4	320	2	Q9XS29	Q9xs29 oryctolagus
18	214.5	9.2	328	2	Q76B99	Q76b99 xenopus lae
19	211.5	9.1	328	2	Q6GLZ4	Q6glz4 xenopus lae
20	206.5	8.9	283	1	TR14_HUMAN	Q92956 homo sapien
21	205	8.8	438	2	Q9DFV0	Q9dfv0 brachydanio
22	203.5	8.8	368	2	Q57408	O57408 meleagris g
23	203.5	8.8	440	1	T10B_HUMAN	O14763 homo sapien
24	200.5	8.6	283	2	Q9XS29	Q9xs28 cercopithec
25	200	8.6	381	1	T10B_MOUSE	Q9qzm4 mus musculus
26	199.5	8.6	335	1	TRN6_HUMAN	P25445 homo sapien
27	199.5	8.6	368	2	Q91AR7	Q91ar7 gallus gall
28	198	8.5	189	2	Q95185	Q95185 felis silve
29	198	8.5	263	2	Q9XS60	Q9xs60 oryctolagus
30	197.5	8.5	276	2	Q71F55	Q71f55 mus musculus
31	197.5	8.5	333	1	TRN6_MACMU	Q9bdp2 macaca mula

32	197	8.5	189	2	O97530	O97530 canis faml
33	197	8.5	327	2	O97491	O97491 ovis aries
34	196.5	8.5	331	2	Q9TSN4	Q9ten4 macaca faec
35	196	8.4	327	1	TRN6_MOUSE	P25446 mus musculus
36	195.5	8.4	275	2	Q80WM9	Q80wm9 mus musculus
37	195.5	8.4	335	2	Q6SS29	Q6sse9 homo sapien
38	193.5	8.3	331	1	TRN6_MACNE	Q9bdn0 macaca neme
39	193	8.3	334	2	Q9GL40	Q9gl40 macaca mula
40	192.5	8.3	323	1	TRN6_BOVIN	P51867 bos taurus
41	191	8.2	321	2	Q6DJ81	Q6dj81 xenopus tro
42	191	8.2	411	1	Q6UXM8	Q6uxm8 homo sapien
43	190.5	8.2	331	1	TRN6_CERTO	Q9bdn4 cercocebus
44	189.5	8.2	368	2	Q9PW79	Q9pw79 gallus gall
45	189	8.1	312	2	Q6E5U7	Q6esu7 ictalurus p

ALIGNMENTS

RESULT 1

ID TR25_HUMAN STANDARD; PRT; 417 AA.

AC O93038; O00275; O00276; O00277; O00278; O00279; O00280; O14865; AC O14866; P78507; P78515; Q29983; Q30306; Q30307; Q99830; AC Q99831; Q9BY86; Q9UME0; Q9UME1; Q9UME5;

DT 01-NOV-1997 (Rel. 35, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DE Tumor necrosis factor receptor superfamily member 25 precursor (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-mediating receptor TRAMP) (Death domain receptor 3) (WSL protein) (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated receptor of death) (LARD) (UNQ455/PRO779).

GN Name=TNFRSF25; Synonyms=APO3, DDR3, DR3, TNFRSF12, WSL, WSL1; OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.

RC TISSUE=Lymphoid;

RX MEDLINE=97088617; PubMed=8934525; DOI=10.1038/384372a0;

RA Kiteon J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T., Grinham C.J., Brown R., Farrow S.N.;

RL "A death-domain-containing receptor that mediates apoptosis.";

RN Nature 384:372-375(1996).

[2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Umbilical vein endothelial cells;

RX MEDLINE=97081063; PubMed=8875942; DOI=10.1126/science.274.5289.990; RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M., Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;

RT "Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95.";

RT Science 274:990-992(1996).

[3]

RN SEQUENCE FROM N.A.

RP Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;

RX Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

[4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Heart;

RX MEDLINE=97148200; PubMed=8994832; DOI=10.1016/S0960-9822(02)70791-4; RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L., Goddard A.D., Bauer K.D., Ashkenazi A.;

RT "Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kappa-B.";

RT Curr. Biol. 6:1669-1676(1996).

[5]

RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).

RP MEDLINE=97272273; PubMed=9114039; DOI=10.1073/pnas.94.9.4615; RX Screaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R., McMichael A.J., Bell J.I.;


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DR EMBL; U94505; AAC51310.1; -
DR EMBL; U94506; AAC51311.1; -
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Best Local Similarity 100.0%; Pred. No. 2.1e-153; Indels 0; Gaps 0;
Matches 417; Conservative 0; Mismatches 0;
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DB 1 MEQPRGCAAAVALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKRP 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKRP 120
QY 121 WFEVQVSCVSSSPFYCQPCDCLGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFEVQVSCVSSSPFYCQPCDCLGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCHWPKPLVTADDEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCHWPKPLVTADDEAG 240
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QY 361 IEAVEVEIGRFRDQOQYEMLRKRWQOQAGLVAVYAALERMGLDGCVEDLRSLQRP 417
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DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE WSL-1-like protein.
GN Name=Tnfrsf25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
EX MEDLINE=21158384; PubMed=11261933; DOI=10.1007/s002510000290;
RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.;
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
RT gene."
RL Immunogenetics 53:59-63(2001).
DR EMBL; AF329969; AAK11256.1; -.
DR HSSP; P19438; 1ICH.
DR MGD; MGI:1934667; Tnfrsf25.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH-like.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac_recept.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
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DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
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Query Match
  60.1%; Score 1397; DB 2; Length 413;
Best Local Similarity 62.9%; Pred. No. 4.6e-89;
Matches 270; Conservative 28; Mismatches 103; Indels 28; Gaps 7;
QY 1 MEQPRGCAAAVALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCP 52
DB 1 MEQPRGCAAAVALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGCP 59
QY 53 AGHYLKAPCTBPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVAD 112
DB 60 KGHYKAPCAEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVAD 119
QY 113 TRCGCKPGWFEVQVSCVSSSPFYCQPCDCLGALHRRHLLCSRRDTCGT---CLPGF 169
DB 120 THCGCQSGWCDCTVPCGKSSPFCVCGATTTPVH-----EAPTRPCLPGF 167
QY 170 YEHGDCVSCPTSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCHW 229
DB 168 YIRGNDCTSCPTGFSVCPKACTAVCGWKQMFVQVLLG---VAFPGAIIICAYCRWQP 224
QY 230 HKPLVTADDEAGWEALTPPPATHLSPLDSAHLLAPDSSSEKIC-TVQLVGNSTWTPGYPET 288
DB 225 CKAVVTADTATEPLASPTAHLSASDSAHLLAPDSSSTGKICTTVQLVGNSTWTPGYSQT 284
QY 289 QEALCPQVTSWTDQPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYVNDVAVPARW 348
DB 285 QEVVCGQASQPDQLENRTLGTPLASPLSPAPPAGSPAALQPGPOLYVNDVAVPARW 344
QY 349 EFVETLGLREAEIEAVEVEIGRFRDQOQYEMLRKRWQOQAGLVAVYAALERMGLDGCVED 408
DB 345 EFVETLGLREAEIEAVEVEIGRFRDQOQYEMLRKRWQOQAGLVAVYAALERMGLDGCVED 404
QY 409 LRSRLQRP 417
DB 405 LRSRLQRP 413
RESULT 3
Q8VD70 PRELIMINARY; PRT; 387 AA.
AC Q8VD70;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tnfrsf25 protein.
GN Name=Tnfrsf25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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FT DISULFID 102 117 By similarity.
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FT DISULFID 185 190 By similarity.
FT CARBOHYD 54 54 N-linked (GlcNAc...) (potential).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (potential).
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Query Match
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Matches 140; Conservative 44; Mismatches 201; Indels 74; Gaps 18;

QY 11 VAAALLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCT 62
DB 14 VLRAALLVDVYAGVHGLVHLFGDREKRESLCPQGKYSHPNRISICTKCHKGTYLHNDCL 73
QY 63 EPCGNSTCLVCPQDFTFLAWENHNSECARCOACDQASQVALENCASAVADTRCGCKPGWF 122
DB 74 GPGLDTRCEDNGTFTASEN-HLTQCLSCSKRSEMSQVEISPTCDRDTVCGCRKN-- 130
QY 123 VECQVSCVSSPPFYCQPCDCLGALHRRHTRLLC-SRRDTCGTCLPGFYEHGDCGVCSCPT 181
DB 131 ---QYRKYWSETLFOCLNCSLCP--NGTVQLPCLEKQDTIC-NCHSGFFLRDKCEKVCSCVN 184
QY 182 STLGCSPERCACVACWRQMP-----WVQVLLAGLVVPLLGLATLTYTRHCHWPH--- 230
DB 185 CKNADCKNLCPATSETRNDFQDTGTVLLPLVIFFGCLAFPLFVGLACRYQRWKPKLYS 244
QY 231 -----KPLATADENAGMEALTPPAPATHLSPD--SAHTLAPPDSEKICTV 274
DB 245 IICGKSTPVKEGEPEPLATAFSG-----PITTFSPISFSPPTTSPVSPSPISPP 297
QY 275 QLVGNWSMT---PGYPETOALCPQVTSWQDQLPSRALGPAAPTLSP-----ESPAG 323
DB 298 TFTPDCWSNIKVTSPPKEIAPPQAG-----PILPMPASTPVPTPLPKWGSAHSAHS 352
QY 324 SPAMMLQGP-QLYVMDAVPARRWKEFVRTLGLREABIEAVEIGR-FRDOQYEMLMKR 381
DB 353 APAQLADADPATLYAVVDGVPPTRWKEFVRRLGLSEHIERLELQNGRCLREAQYSLAE 412
QY 382 WRQ---QQPAGIGAVYAALERMGLDGCVEDLRSRLQGP 417
DB 413 WRRRTSRREATLELGLSVLRMDMLGCLDEDIEAL-RGP 450

RESULT 5
Q6QHF0
ID Q6QHF0 PRELIMINARY; PRT; 440 AA.
AC Q6QHF0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE TNF receptor superfamily, member 1A (Fragment).
GN Name=Thfsfla;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Jico; TISSUE=Liver;
RA Staelens J., Wielockx B., Puimege L., Vandenabeele A., Libert C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV541590; AAS48429.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0036021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
```

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DR GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR GO; GO:0008219; P:cell death; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu...; IMP.
DR GO; GO:0006952; P:defense response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR GO; GO:0007515; P:lymph gland development; IMP.
DR GO; GO:0006693; P:prostaglandin metabolism; TAS.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 440 440
SQ SEQUENCE 440 AA; 48639 MW; D343ED449B260188 CRC64;

Query Match
Best Local Similarity 17.5%; Score 406.5; DB 2; Length 440;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;

QY 11 VAAALLLVLLGARAQGGT-----RSPRCDCAGDFHKKIGLFCRCGCPAGHYLKA 59
DB 5 LSLVLLALLMGHISHSVGTGLVPSLGDREKRDLSLCPQGKYVHSKNSICTCKHGTLYLS 64
QY 60 PCTPCCGNSTCLVCPQDFTFLAWENHNSECARCOACDQASQVALENCASAVADTRCGCKP 119
DB 65 DCPSPGRDVTVCRECEKGTFTASQNYLR-QCLSCKTCRKEMSQVEISPCQADKDTVCGCK- 122
QY 120 GMFVECVQSCVSSPPFYCQPCDCLGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVCSC 179
DB 123 ---ENQFQYLSSTHFCQVDCSC--FNGVTVPCKETQNTVNCNCHAGFFLRSECVPC 176
QY 180 PTSTLIGSCP--ERCAAVC-----GWRQMFVWVQLLAGLVVPLLGLATLTYT 224
DB 177 -----SHCKKNECKMLCLPPLANVTNPQDSGTAVLLVLLGLCLLSFIFSLMCRY 231
QY 225 RHCWP-----HKPLVTADENAGMEALTPPAPATHLSPDLSAHTLL-----APDSEK 270
DB 232 PRWRPEVYIIICRDPVPVKEEKAGKPLTPAPSPAFSPSTSGFNFTLGFSTPGFSSPVSTP 291
QY 271 ICTVLQVGNWS-----TPGY-PETOEALC---PQVTSWQDQLPSRALGPAAP 314
DB 292 ISPI-FGFSNWHXMPVSEVVPTQADPLLYESLCFVPAPTSVQKNE----- 338
QY 315 TLPSPSPAGSPAMMLQGPQLYVMDAVPARRWKEFVRTLGLREABIEAVEIGR-FRD 373
DB 339 SAHQRPVNAADLAI-----LYAVVDGVPVPAWKEMFMRMGLSEHIERLEMQNGRCLRE 392
QY 374 QOYEMLMKRQOQPA---GLGAVVAALERMGLDGCVEDLRSRLQGP 417
DB 393 AQYSMLAEAWRRRTPRHEDTLEVVGLVLSKNNLAGCLNLEAL-RNP 438

RESULT 6
Q6QHF2
ID Q6QHF2 PRELIMINARY; PRT; 440 AA.
AC Q6QHF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TNF receptor superfamily, member 1A (Fragment).
```



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DR Pfam; PF00020; TNFR_C6; 4.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS0052; TNFR_NGR1; 3.
DR PROSITE; PS0050; TNFR_NGR2; 3.
KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 454 Tumor necrosis factor receptor
FT FT superfamily member 1A.
FT FT Extracellular (Potential).
FT FT POTENTIAL.
FT FT 212 212
FT FT TRANSMEM 213 235
FT FT DOMAIN 236 454
FT FT REPEAT 43 82
FT FT REPEAT 83 125
FT FT REPEAT 126 166
FT FT REPEAT 167 196
FT FT DOMAIN 339 349
FT FT DOMAIN 356 441
FT FT DISULFID 44 58
FT FT DISULFID 59 72
FT FT DISULFID 62 81
FT FT DISULFID 84 99
FT FT DISULFID 102 117
FT FT DISULFID 105 125
FT FT DISULFID 127 143
FT FT DISULFID 146 158
FT FT DISULFID 149 166
FT FT DISULFID 168 179
FT FT DISULFID 182 195
FT FT DISULFID 185 191
FT FT CARBOHYD 54 54
FT FT CARBOHYD 151 151
FT FT CARBOHYD 202 202
FT FT CONFLICT 394 394
FT FT CONFLICT 394 394
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C286D9 CRC64;

Query Match 17.4%; Score 404.5; DB 1; Length 454;
Best Local Similarity 27.2%; Pred. No. 4.7e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 16;

Qy 11 VAAALLVLLGARAQGGT-----RSPRCDCAGDFHKKGLFCRCPCPAGHYLKA 59
Db 11 LSLVLLALLGHHGSGVGLVPSLGDREKRSCLPQGGKYVHSKNNISCTCKHGTLYLS 70
Qy 60 PCTBPCGNSTCLVCPQDTFFLAWENHNSECARQACDEQAQVALENGSAVADTRCGCKP 119
Db 71 DCPSPGRDTCRECEKGTFTASQVLR-QCLSKCTCRKMSQVLSPCQADKDTVCCKX- 128
Qy 120 GWFEVCQVSSPFFYQPCQLDGLHRRHLLCSRRDTDCGTCLPGFYEHGDCGVSC 179
Db 129 ----ENQFQVLSETHFQVDCSPC--PNGVTTPICKETQNTVCNCHAGFFLRESECVPC 182
Qy 180 PTLTSLGSCP--ERCAAVC-----GWQMFVQVLLAGLVVPLLGLATLITY 224
Db 183 ----SHCKNKECKMLCPPLANVTNPQDSGTAVLLPLVLLGLCLLSFIFSLMCRY 237
Qy 225 RHQWP-----HKPLVTADEAGMEALTPPPTHLSPLDSAHLL-----APPDSSEK 270
Db 238 PRWRPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSTSGFNPLTGFSTPGFSPVSTP 297
Qy 271 ICTVLQVNSW-----TPGY-PETQALC-----PQVTSWDLPSRALGPAAP 314
Db 298 ISPI-FGSPNNHFMPPVSEVPTQCADPLLYESLCSVPAPTSQVKWED----- 344
Qy 315 TSLSPSPAGSPAMMLQPGPOLQYDMDVAPARRWKEFVPTLGLREAEIYAVEVEIGR-PRD 373
Db 345 SAHPORPNADLAI-----LYAVVDGVPAPRWKEFMFMFGLSHEHIEIRLEMQNRCURE 398
Qy 374 QQYEMLKRWQOQPA--GLGAVAAALERMGLDGCVEDLRSRLQKGP 417
Db 399 AQYSMLEAWRRRTPRHEDTLEVVGLVLSKMNLAGLENILEAL-RNP 444

RESULT 9
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```
TR1A RAT
ID TR1A RAT STANDARD; PRT; 461 AA.
AC P22934; Q91V30; Q91V93;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN Name=TNfrsfla; Synonym=TNfr-1, TNfr1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
MEDLINE=91090841; PubMed=1702293;
RA Hammler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor necrosis
RT factor-binding protein."
RL DNA Cell Biol. 9:705-715(1990).
[2]
RN SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC STRAIN=ACI/Seghshd, BB(DR)/Wor, BN/SSNHsd, DA/Bkl, F344/NHsd, and
RC LEW/NHsd;
RA Furuya T., Saitstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,
RA Wilder R.L., Remmers E.F.;
RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT among autoimmune susceptible and resistant inbred rat strains."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAGA (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
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DR EMBL; M63122; AAA42256.1; -.
DR EMBL; AF329976; AAK53562.1; -.
DR EMBL; AF329977; AAK53563.1; -.
DR EMBL; AF329981; AAK53567.1; -.
DR EMBL; AF329978; AAK53564.1; -.
DR EMBL; AF329979; AAK53565.1; -.
DR EMBL; AF329980; AAK53566.1; -.
DR PIR; B36555; GQRTT1.
DR HSP; P19438; LICH.
DR RGD; 621237; TNfrsfla.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.
```

DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential
FT CHAIN 22 461 Tumor necrosis factor receptor
FT superfamily member 1A.
FT EXTRACELLULAR (Potential).
FT POTENTIAL.
FT TRANSMEM
FT DOMAIN 22 211
FT DOMAIN 212 234
FT DOMAIN 235 461 Cytoplasmic (Potential).
FT REPEAT 43 82 TNFR-Cys 1.
FT REPEAT 83 125 TNFR-Cys 2.
FT REPEAT 126 166 TNFR-Cys 3.
FT REPEAT 167 196 TNFR-Cys 4.
FT DOMAIN 344 354 N-SMase activation domain (NSD).
FT DOMAIN 363 448 Death.
FT DISULFID 44 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 81 By similarity.
FT DISULFID 84 99 By similarity.
FT DISULFID 102 117 By similarity.
FT DISULFID 105 125 By similarity.
FT DISULFID 127 143 By similarity.
FT DISULFID 146 158 By similarity.
FT DISULFID 149 166 By similarity.
FT DISULFID 168 179 By similarity.
FT DISULFID 182 195 By similarity.
FT DISULFID 185 191 By similarity.
FT CARBOHYD 54 54 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 151 151 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 201 201 N-linked (GLCNAC. .) (Potential).
FT VARIANT 230 230 I -> V (in strain LEW/NHsd, strain ACI/
SegHsd, strain DA/Bkl and strain F344/
NHsd).
FT VARIANT 295 295 H -> P (in strain LEW/NHsd, strain ACI/
SegHsd, strain DA/Bkl, strain F344/NHsd
and strain BN/SsnHsd).
SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;
Query Match 17.0%; Score 394.5; DB 1; Length 461;
Best Local Similarity 27.9%; Pred. No. 2.3e-19;
Matches 128; Conservative 55; Mismatches 202; Indels 73; Gaps 18;
QY 11 VAAALLVLLGARAQ-----GTRSPR---CDACGDFHKKIGLFCRCGCPAGHYLKA 59
DB 11 LSLVLLALLMGHPGVTGLVPSLGDREKRNLCPOGKYAHPKXNSICTCKHKGTYLVS 70
QY 60 PCTPCGNSCLVCPQDTFLAWENHNSEACQACDEQASQVALENCASAVADTRCGCKP 119
DB 71 DCPSPGQETVCEVCDKGTFTASQNHVR-QCLSKCTCKEMFQVEISPCKADMDTVCGCK 129
QY 120 GWFEVCQVSSSFFVCQCLDCGALHRRHRLTLLCSRRDTCGTLCPGFVEHGGCVSC 179
DB 130 N-----QFQYLSETHFOCVDCSPC--FNGVTTPCKEKQNTVCNCHAGFLSGNNECTPC 182
QY 180 PTSTLGSCLP--ERCAAVC-----GWROMFWQVLLAGLAVPPLLGLATLTYR 225
DB 183 -----SHCKKQECMKCLPVPVANTPNQDSGTAVLLPLVFLGLCLLFFICISLLCRYP 237
QY 226 H-----CWPXKPLVTADEAGM--BALTPPPATHLSPLDSAHLL-----APPD 266
DB 238 QWRPRVYSIIICRDSAPVKEVEGEGIVTKPLTPASIPAFSPNPGFNPTLFGSTTFRFSHPV 297
QY 267 SSEKICTVQLVGNSTPGYPETOALCPQVTSWDQLPSRALGPAAATLSP-----ESP 321
DB 298 SSTPISPV-FGFSNWHNVFPVPPREVY---PTQADPLLYGSLNPVPIP--APVRKWDVW 351
QY 322 AGSPAMMLQPGP-QLYDVMDVAPARRWKEFVRLTLGLREAEVAVEIGR-FRDOQYBML 379
DB 352 AAQPORLTDAPMLYAVVDGVPPTRWKEFRLGLSHEIERLQLQRCRLREAHYML 411
QY 380 KRWROQOP---AGLGAVYAALERMLDGCVEDLRSRLQ 414

DB 412 EAWRRRTPRHEATLDVVGRLCDMLNGLGLENIRETLE 449
RESULT 10
TR1A_BOVIN STANDARD; PRT; 471 AA.
ID TRIA_BOVIN AC 019131;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-RI) (TNF-RI) (p55).
GN Name=TNFRSF1A; Synonyms=TNFR1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98273505; PubMed=9613449; DOI=10.1016/S0165-2427(97)00136-0;
RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;
RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor
Vet. Immunol. Immunopathol. 61:379-385(1998).
CC -!- FUNCTION: Receptor for TNFSP2/TNF-alpha and homotrimeric
TNFSP1/lymphotoxin-alpha. The adaptor molecule FADD recruits
caspase-8 to the activated receptor. The resulting death-inducing
signaling complex (DISC) performs caspase-8 proteolytic activation
which initiates the subsequent cascade of caspases (aspartate-
specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: Binding of TNF to the extracellular domain leads to a
homotrimerization. The aggregated death domains provide a novel
molecular interface that interacts specifically with the death
domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
RIP and possibly FADD, are recruited to the complex by their
association with TRADD. This complex activates at least two
distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAC4. Constitutively associated with TRPC4AP (By
similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-
terminal region containing the death domain are involved in the
interaction with TRPC4AP (By similarity).
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sib.ac.uk).
EMBL; U90937; AB65143.1; --
HSP; P19438; IICH.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR000488; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00531; Death; 1.
Pfam; PF00020; TNFR_C6; 3.
PRINTS; PR00353; 4Fe4SPROXIN.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS0017; DEATH DOMAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential.

```
FT CHAIN 22 471 Tumor necrosis factor receptor
FT DOMAIN 22 210 superfamily member 1A.
FT TRANSMEM 211 233 Extracellular (Potential).
FT DOMAIN 234 471 Potential
FT REPEAT 43 82 Cytoplasmic (Potential).
FT REPEAT 83 125 TNFR-Cys 1.
FT REPEAT 126 166 TNFR-Cys 2.
FT REPEAT 167 195 TNFR-Cys 3.
FT REPEAT 196 340 TNFR-Cys 4.
FT DOMAIN 340 360 N-SHase activation domain (NSD).
FT DOMAIN 372 457 Death.
FT DISULFID 44 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 81 By similarity.
FT DISULFID 84 99 By similarity.
FT DISULFID 102 117 By similarity.
FT DISULFID 105 125 By similarity.
FT DISULFID 127 143 By similarity.
FT DISULFID 146 158 By similarity.
FT DISULFID 149 166 By similarity.
FT DISULFID 168 179 By similarity.
FT DISULFID 182 194 By similarity.
FT DISULFID 185 190 By similarity.
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 471 AA; 51367 MW; 5243BF514DFB81C4 CRC64;

Query Match 16.7%; Score 387.5; DB 1; Length 471;
Best Local Similarity 26.9%; Pred. No. 7.3e-19;
Matches 130; Conservative 47; Mismatches 186; Indels 121; Gaps 18;

QY 11 VAAALLLLGARAGGGTRSPRCACAGDF-----HKIGLFCRCGCPAGHYL 57
Db 14 VLPALLADVPAGVQGLVPH-----GDLEKRESPCGKGNHFNQNTICCKHGYYL 68
QY 58 KAPCTEPCGNCSTLCVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCG 117
Db 69 YNDCPGPGRDTCRCVAPGTVTALENHLR-RCLSCSRCRDEMFOVEISPCVVDRTVCGC 127
QY 118 KPGHFEVCQVSSSPFYCPCLDC--GALHRRHLRLC-SRDTDCGTCLPGFYEHGD 174
Db 128 RKN-----QYREYWGEGTFRCLNCSLCPNGTVN----IPCQERQDTTC-HCHMGFFLKGA 177
QY 175 GCVSCPTSLTSCPER-CAAVCGWR-----QMFVQVLLAGLVVPLLLGATLT 221
Db 178 KCISC-----HDCNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLA 232
QY 222 YTYRHCWPHK-----PLVT 235
Db 233 CRYQR-WKPKLYSIICGQSTLVKEGEPPELLVPAPGNFTTTCFSSPTSSPVSIPPVIS 291
QY 236 ADEAGMEALTTPPATHLSPLDSANTLLAPPSSSEKICTVQLVGNSS--WTPGYPTQALC 293
Db 292 CDRENFGAVAPSSSETAPPHLKAGPILPGPPASTHLCTCPGPPASTHLCTCPGPPASTHLCT 351
QY 294 FOVTWSNDQLSRALGAAAFTLPSPESAPGAMMLQPGPOLYDVMDAVPARRKKEFVRT 353
Db 352 PVQKW-----EASAPSAQPOLADADPA-----TLYAVDVGVPSPRWKELVRR 393
QY 354 LGLREAEIAEVEIGR-FRQOQYEMLRKWRQQQP---AGLGAVYAALERMGLDGCVEDL 409
Db 394 LGLSEHEIERLENGRHLREAQYSLAAWRRRTPRREATUELLGRVLRDMDLLGCLNI 453
QY 410 RSRL 413
Db 454 EEAL 457

RESULT 11
TRIA_HUMAN
ID TRIA_HUMAN STANDARD; PRT; 455 AA.
AC P19438;
```

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DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor
DE binding protein 1 (TBPI)].
DE Name=TNFRSF1A; Synonyms=TNFAR, TNFR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RC MEDLINE=90235285; PubMed=2158863;
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,
RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT "Molecular cloning and expression of a receptor for human tumor
RT necrosis factor.";
RL Cell 61:361-370(1990).
RN [2]
RN SEQUENCE FROM N.A.
RC MEDLINE=90235284; PubMed=2158862;
RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
RT factor receptor.";
RL Cell 61:351-359(1990).
RN [3]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RC MEDLINE=91006021; PubMed=1698610;
RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA Aderka D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT for the type I TNF-R, cloned using amino acid sequence data of its
RT soluble form, encodes both the cell surface and a soluble form of the
RT receptor.";
RL EMBO J. 9:3269-3278(1990).
RN [4]
RN SEQUENCE FROM N.A.
RC MEDLINE=91090841; PubMed=1702293;
RA Hammler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor necrosis
RT factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RC MEDLINE=91017509; PubMed=2170974;
RA Gray P.W., Barrett K., Chantray D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT expression of recombinant soluble TNF-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN [6]
RN SEQUENCE FROM N.A.
RC MEDLINE=92250049; PubMed=1315717;
RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.;
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT localization to chromosome 12p13.";
RL Genomics 13:219-224(1992).
RN [7]
RN SEQUENCE FROM N.A., AND VARIANTS LEU-75 AND GLN-121.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL6682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
```


RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paney J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Trichman J.W., Green E.D., Dickens M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[9]
RP SEQUENCE OF 41-45.
RP MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human urine.
RT Evidence for immunological cross-reactivity with cell surface tumor
RT necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
[10]
RP INTERACTION WITH BAG4.
RP MEDLINE=91115917; PubMed=9915703; DOI=10.1126/science.283.5401.543;
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of
RT death domains.";
RL Science 283:543-546(1999).
[11]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFBS.
RP MEDLINE=93258809; PubMed=8387891; DOI=10.1016/0092-8674(93)90132-A;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445(1993).
[12]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RP MEDLINE=97094982; PubMed=8939750;
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
RT "Structures of the extracellular domain of the type I tumor necrosis
RT factor receptor.";
RL Structure 4:1251-1262(1996).
[13]
RP VARIANTS FHF ARG-59; TYR-79; PHE-81; ARG-117 AND TYR-117.
RA MEDLINE=99213501; PubMed=1019409; DOI=10.1016/S0092-8674(00)80721-7;
RA McDermott M.F., Akseentjevich I., Galon J., McDermott E.M.,
RA Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L.,
RA Petherick T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,
RA Teppo A.-M., Wilson M., Karaaslan H.M., Wan Y., Todd I., Wood G.,
RA Schlimgen R., Kumarjeeva T.R., Cooper S.M., Vella J.P., Amos C.I.,
RA Mulley J., Quane K.A., Molloy M.G., Knaki A., Powell R.J.,
RA Hitman G.A., O'Shea J., Kastner D.L.;
RT "Germline mutations in the extracellular domains of the 55 kDa TNF
RT receptor, TNFR1, define a family of dominantly inherited
RT autoinflammatory syndromes.";
RL Cell 97:133-144(1999).
[14]
RP VARIANT FHF SER-59.
RA PubMed=10902757;
RA Dode C., Papo T., Fieschi C., Pecheux C., Dion E., Picard F.,
RA Godeau P., Bienvenu J., Piette J.C., Delpech M., Grateau G.;
RT "A novel missense mutation (C30S) in the gene encoding tumor necrosis
RT factor receptor 1 linked to autosomal-dominant recurrent fever with
RT localized myositis in a French family.";
RL Arthritis Rheum. 43:1535-1542(2000).

RN VARIANTS FHF GLN-51; SER-59; GLY-62; LEU-75; GLY-115 AND GLN-121.
RX PubMed=11443543;
RA Akseentjevich I., Galon J., Soares M., Mansfield E., Hull K.,
RA Oh H.-H., Goldbach-Mansky R., Dean J., Athreya B., Reginato A.J.,
RA Henrickson M., Fong-Estel B., O'Shea J.J., Kastner D.L.;
RT "The tumor-necrosis-factor receptor-associated periodic syndrome: new
RT mutations in TNFRSF1A, ancestral origins, genotype-phenotype studies,
RT and evidence for further genetic heterogeneity of periodic fevers.";
RL Am. J. Hum. Genet. 69:301-314(2001).
[16]
RP VARIANTS FHF SER-99 AND PRO-121.
RX PubMed=13130484; DOI=10.1002/art.11215;
RA Aganna E., Hammond L., Hawkins P.N., Aldea A., McKee S.A.,
RA Ploos van Amstel H.K., Mischung C., Kusuha K., Saulsbury F.T.,
RA Lachmann H.J., Bybee A., McDermott E.M., La Regina M., Arostegui J.I.,
RA Campistol J.M., Worthington S., High K.P., Molloy M.G., Baker N.,
RA Bidwell J.L., Castaner J.L., Whiteford M.L., Janssens-Korpola P.L.,
RA Manna R., Powell R.J., Woo P., Solis P., Minden K., Frenkel J.,
RA Yague J., Mirakian R.M., Hitman G.A., McDermott M.F.;
RT "Heterogeneity among patients with tumor necrosis factor receptor-
RT associated periodic syndrome phenotypes.";
RL Arthritis Rheum. 48:2632-2644(2003).
[17]
RP VARIANT FHF SER-99.
RX PubMed=14610673; DOI=10.1007/s00431-003-1338-0;
RA Kusuha K., Nomura A., Nakao F., Hara T.;
RT "Tumor necrosis factor receptor-associated periodic syndrome with a
RT novel mutation in the TNFRSF1A gene in a Japanese family.";
RL Eur. J. Pediatr. 163:30-32(2004).
CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis. Contributes to
CC the induction of noncytotoxic TNF effects including anti-viral
CC SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAG4. Constitutively associated with TRPC4AP (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -!- DOMAIN: The domain that induces A-SMASE is probably identical to
CC the death domain. The N-SMASE activation domain (NSD) is both
CC necessary and sufficient for activation of N-SMASE.
CC -!- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-
Query March 16.1%; Score 374; DB 1; Length 455;
Best Local Similarity 28.3%; Pred. No. 6.1e-18;
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;
QY 15 LLLVLLGARAQG-----GTRSPR---CDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
DB 15 LLELVGLYPSGVGLVPLHGLDRKRSVCGPGKYVHPQNNISICTCKHGTLYNDPCG 74
QY 64 PCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQAQVALENCASAVADTRCGCKPGWV 123
DB 75 PGQDTRCECSGSFTASENHLR-HCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQYR 133
QY 124 EC---QVSQCVSSFFFCQPCLDGALHRRHLLCSRDRDTCGCLPFGYHGDGCVSCP 180
DB 134 HWSENLFQ-----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFURENECVSC- 182
QY 181 TSTLGSCPE--RCAAVC-----GWRQMFQVQLLAGLVPLLLGATITYYRH 226
DB 183 ----SNCKSLECKLCLPQIENVKGTEDSGTVLLPLVIFFGLLSLLFGLMYRQYR 238

[illegible]

Euteleostomi;
 i; Cypriniformes;
 1.242603899;
 J.G.,
 I., Schuler G.D.,
 F., Bhat N.K.,
 I., Hsieh P.,
 , Hong L.,
 I.L., Schetz T.E.,
 P., Prange C.,
 I.D., Mullahy S.J.,
 Gunaratne P.H.,

Euteleostomi;
Cypriniformes;
J.G.,
Schulz G.D.,
Bhat N.K.,
Hsieh F.,
Hong L.,
L., Scheetz T.E.,
P., Prange C.,
D., Mullahy S.J.,
Gunaratne P.H.,

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:37:14 ; Search time 164 Seconds
(without alignments)
983.409 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323
Sequence: 1 MEQPRGCAVAAALLLVLL.....ERMGLDGCVEDLRSLRQGP 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003s:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	417	2 AAW31517	Aaw31517 Death dom
2	2323	100.0	417	2 AAW26709	Aaw26709 Human apo
3	2323	100.0	417	2 AAW57045	Aaw57045 Human apo
4	2323	100.0	417	2 AAW95538	Aaw95538 Death dom
5	2323	100.0	417	2 AAY05743	Aay05743 Tumour ne
6	2323	100.0	417	3 AAB36265	Aab36265 Human dea
7	2323	100.0	417	4 AAB97370	Aab97370 Human the
8	2323	100.0	417	5 AAO17879	Aao17879 Human the
9	2323	100.0	417	5 AAU86139	Aau86139 Human PRO
10	2323	100.0	417	6 ABG73993	Abg73993 Human Apo
11	2323	100.0	417	6 ABU08252	Abu08252 Human Apo
12	2323	100.0	417	6 ABG73859	Abg73859 Human Apo
13	2323	100.0	417	6 ABU10204	Abu10204 Human Apo
14	2323	100.0	417	6 ADA00738	Ada00738 Human GEN
15	2323	100.0	417	6 ABG73824	Abg73824 Human apo
16	2323	100.0	417	6 ADA49692	Ada49692 Human Apo
17	2323	100.0	417	7 ABW02265	Abw02265 Human TNF
18	2323	100.0	417	7 ADG88381	Adg88381 Human dea
19	2323	100.0	417	7 ADJ37305	Adj37305 Human tum
20	2323	100.0	417	7 ADN95869	Adn95869 Human BEC
21	2323	100.0	417	8 ADH34623	Adh34623 TNF recep
22	2323	100.0	417	8 ADG68229	Adg68229 Human PRO
23	2323	100.0	417	8 ADL27893	Adl27893 Human dea
24	2323	100.0	417	8 ADQ16568	Adq16568 Human dea
25	2323	100.0	417	8 ADQ59120	Adq59120 Human dea

26	2323	100.0	418	4 AAB84941	Aab84941 Amino aci
27	2323	100.0	418	8 ADH50948	Adh50948 Human dea
28	2323	100.0	833	2 AAW64486	Aaw64486 Human DR3
29	2308.5	99.4	416	6 ABG73995	Abg73995 Human Apo
30	2308.5	99.4	416	6 ABG73862	Abg73862 Human Apo
31	2306	99.3	417	7 ADL15011	Adl15011 Human WSL
32	2292	98.7	451	8 ABM84914	Abm84914 Human dia
33	2277.5	98.0	450	8 ABM84915	Abm84915 Human dia
34	2267	97.6	428	2 AAW31516	Aaw31516 Death dom
35	2267	97.6	428	2 AAW95537	Aaw95537 Death dom
36	2267	97.6	428	3 AAB36264	Aab36264 Human dea
37	2267	97.6	428	7 ADG88379	Adg88379 Human DR3
38	2267	97.6	428	8 ADL27891	Adl27891 Human Dea
39	2179.5	93.8	426	3 AAB01337	Aab01337 TNF recep
40	1862	80.2	343	4 AAB50918	Aab50918 Human PRO
41	1404	60.4	411	2 AAW57046	Aaw57046 Mouse apo
42	1164	50.1	253	7 ADL15009	Adl15009 Human WSL
43	1052.5	45.3	218	7 ADL15010	Adl15010 Human WSL
44	1051	45.2	181	2 AAW26708	Aaw26708 Human Apo
45	1051	45.2	181	6 ABG73992	Abg73992 Human Apo

ALIGNMENTS

RESULT 1
AAW31517
ID AAW31517 standard; protein; 417 AA.
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AC AAW31517;
XX
DT 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3.
XX
KW Death domain containing receptor; DR3-V1; human; apoptosis; inflammation;
KW NF-kappaB.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Domain /label= Sig_peptide
FT Domain 25..201
FT Domain /note= "extracellular domain"
FT Domain 202..224
FT Domain /note= "transmembrane domain"
FT Domain 225..417
FT Domain /note= "intracellular domain"
FT Domain 342..408
FT Domain /note= "death domain"
XX
WO9733904-A1.
PD 18-SEP-1997.
XX
XX 17-OCT-1996; 96WO-US016849.
XX 12-MAR-1996; 96US-0013285P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX Yu G, Ni J, Dixit VM, Gentz RL, Dillon PJ;
XX WPI; 1997-470812/43.
XX N-FSDB; AAT89427.
XX
XX Death domain containing receptor polypeptide(s) DR3 and DR3-V2 - for
XX activation of apoptosis and NF-kappaB, antagonists can be used to treat
XX inflammatory diseases.
XX Claim 1; Page 75-77; 108pp; English.
PS

```
XX This protein comprises human death domain containing receptor DR3, a
CC novel member of the tumour necrosis factor receptor family. Its amino
CC acid sequence was deduced from a cDNA clone (see AAT89427) isolated from
CC a HUVEC cDNA library. Related death domain containing receptor DR3-V1
CC (see AAW31516) has also been identified. Recombinant full-length or
CC mature DR3, or the extracellular, transmembrane, intracellular or death
CC domain of DR3 can be expressed in transfected host cells. These
CC polypeptides can be used to treat diseases and disorders associated with
CC the inhibition of apoptosis, or to screen for modulator compounds.
CC Antagonists, such as antibodies raised against DR3-V1, can be used to
CC treat diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders
XX
XX Sequence 417 AA;

Query Match      100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAVAAALLLVLLGNARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAVAAALLLVLLGNARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVSCVSSSPFYCQCLDCGALHRLTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVEQVSCVSSSPFYCQCLDCGALHRLTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCHWPKPLVTAD EAG 240
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QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWTPGYPTQ EALCPQV TWSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWTPGYPTQ EALCPQV TWSW 300
QY 301 DQPSRALGPAAATPLSPESPA GSPAMMLQPGPOLYVMDAVPARRWKEFVRTI GLREAE 360
Db 301 DQPSRALGPAAATPLSPESPA GSPAMMLQPGPOLYVMDAVPARRWKEFVRTI GLREAE 360
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Db 361 IEAVEVEIGRFRDQDYEMLKWRQOOPAGLGAVVAALERMGLDGCVEDLRSRLQRP 417

RESULT 2
AAW26709
ID AAW26709 standard; protein; 417 AA.
XX AC
XX AC
XX AC
XX AAW26709;
XX 14-APR-1998 (first entry)
XX Human apoptosis protein Apo-3.
XX Apo-3; apoptosis; human; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..24
XX FT /label= Sig_peptide
XX FT 25..198
XX FT /note= "extracellular domain"
XX FT Modified-site 67
XX FT /note= "N-glycosylated"
XX FT Modified-site 106
XX FT /note= "N-glycosylated"
XX FT 199..224
XX FT Domain
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FT Domain /note= "transmembrane domain"
FT 225..417
FT Domain /note= "intracellular domain"
FT 338..417
XX /note= "death domain"
XX WO9737020-A1.
XX 09-OCT-1997.
XX 31-MAR-1997; 97WO-US005230.
XX 01-APR-1996; 96US-00625328.
XX 23-SEP-1996; 96US-00710802.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI; 1997-503105/46.
XX N-FSDB; AAT91180.
XX Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis in
XX mammalian cells.
XX Claim 19; Page 46-48; 70pp; English.
XX This novel polypeptide, designated Apo-3, is a protein that stimulates or
XX induces apoptotic activity in mammalian cells purposes. Its amino acid
XX sequence was deduced from a human foetal heart cDNA clone (see AAT91180).
XX The N-terminal 181 amino acids of Apo-3 are identical to the sequence of
XX another novel apoptosis polypeptide, Apo-2LI (see AAW26709). Also claimed
XX are: polypeptides comprising the extracellular or death domain of Apo-3;
XX chimeric molecules comprising Apo-3 fused to a heterologous amino acid
XX sequence; antibodies that bind to Apo-3 or its extracellular domain;
XX nucleic acids encoding the polypeptides, as well as vectors and host
XX cells; a non-human transgenic animal containing cells that express
XX nucleic acid encoding Apo-3; and a non-human knockout animal containing
XX cells having an altered Apo-3 gene. Apo-3 can be used to induce apoptosis
XX or NF-kappa-B- (NF-kB) - or JNK-mediated gene expression for therapeutic
XX purposes. Apo-3-IgG fusion proteins can be used to inhibit apoptosis or
XX NF-kB induction or JNK activation for therapeutic purposes, and can be
XX used as immunogens for anti-Apo-3- antibody production. Apo-3 or Apo-2LI
XX can also be used as assay standards. The animals can be used in drug
XX screening and development
XX
XX Sequence 417 AA;

Query Match      100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAVAAALLLVLLGNARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAVAAALLLVLLGNARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVSCVSSSPFYCQCLDCGALHRLTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVEQVSCVSSSPFYCQCLDCGALHRLTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCHWPKPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCHWPKPLVTAD EAG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWTPGYPTQ EALCPQV TWSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWTPGYPTQ EALCPQV TWSW 300
QY 301 DQPSRALGPAAATPLSPESPA GSPAMMLQPGPOLYVMDAVPARRWKEFVRTI GLREAE 360
Db 301 DQPSRALGPAAATPLSPESPA GSPAMMLQPGPOLYVMDAVPARRWKEFVRTI GLREAE 360
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Db 301 DQPSRALGPAAPTSLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
QY 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417

RESULT 3
AAW57045
ID AAW57045 standard; protein; 417 AA.
XX
AC AAW57045;
XX
DT 20-AUG-1998 (first entry)
XX
DE Human apoptosis inducing receptor.
XX
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW Type I transmembrane protein; tumour cell death; autoimmune disease;
KW therapy.
XX
OS Homo sapiens.
XX
FW WO9814565-A1.
XX
PD 09-APR-1998.
XX
PF 03-OCT-1997; 97MO-US017876.
XX
PR 04-OCT-1996; 96US-0044456P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Perkins PA;
XX
DR WPI; 1998-240077/21.
DR N-PSDB; AAV28700.
XX
PT DNA encoding apoptosis inducing receptor - which is Type I transmembrane
PT protein, useful for regulating cell death.
XX
PS Claim 16; Page 28-30; 45pp; English.
XX
CC This sequence is the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAVAAALLLVLLGARAQGGTRSPRCDGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAVAAALLLVLLGARAQGGTRSPRCDGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPDPTFLAENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPDPTFLAENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSSPFYQPCPLDCGALHRRHTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVEQVQSCVSSSPFYQPCPLDCGALHRRHTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADSEAG 240

Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADSEAG 240
QY 241 MEALTTPPATHSLSDSAHTLLAPPDSSEKICTVOLGNSWTPGYPETOEALCPQVTTWSW 300
Db 241 MEALTTPPATHSLSDSAHTLLAPPDSSEKICTVOLGNSWTPGYPETOEALCPQVTTWSW 300
QY 301 DQPSRALGPAAPTSLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQPSRALGPAAPTSLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
QY 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417

RESULT 4
AAW95538
ID AAW95538 standard; protein; 417 AA.
XX
AC AAW95538;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3).
XX
KW Death domain; receptor; DR3-V1; DR3; recombinant.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1. .24 Location/Qualifiers
FT Protein 25. .417 /note= "signal peptide"
FT /note= "mature protein"
XX
FN JP11000170-A.
XX
PD 06-JAN-1999.
XX
PF 12-MAR-1997; 97JP-00057503.
XX
PR 12-MAR-1996; 96US-0013285P.
PR 17-OCT-1996; 96US-0028711P.
PR 06-FEB-1997; 97US-0037341P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
DR WPI; 1999-124390/11.
DR N-PSDB; AAX00925.
XX
PT New death domain containing receptor and recombinant vector - optionally
PT comprising leader sequence.
XX
PS Claim 1; Fig 3; 50pp; Japanese.
XX
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is
CC contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are used
CC for the recombinant production of the proteins. The present sequence
CC represents the amino acid sequence of a death domain containing receptor
CC polypeptide (DR3)
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAAVAAALLLVLLGARAQGGTRSPRCDGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGCLPGFYEHGDCVSCP 180
Db 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADDEAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTWPGYPETQEALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTWPGYPETQEALCPQVTSW 300
Qy 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQRP 417

RESULT 5
AAY05743
ID AAY05743 standard; protein; 417 AA.
AC AAY05743;
XX
DT 19-JUL-1999 (first entry)
DE Tumour necrosis factor receptor TR3.
XX
KW Tumour necrosis factor receptor; TR3; DR3; Apo3; WSL-1; LARD; agonist;
KW antagonist; screening; human; Alzheimer's disease; AIDS; cancer;
KW inflammation; arthritis; septicaemia; autoimmune disease; psoriasis;
KW inflammatory bowel disease; transplant rejection;
KW graft versus host disease; infection; stroke; ischaemia;
KW acute respiratory disease syndrome; restenosis; brain injury;
KW bone disease; atherosclerosis; therapy.
XX
OS Homo sapiens.
XX
FN EP911633-A1.
XX
PD 28-APR-1999.
XX
PF 02-OCT-1998; 98EP-00203332.
XX
PR 08-OCT-1997; 97US-0061334P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI McDonnell PC, Young PR, Zou J;
XX
DR WPI; 1999-246560/21.
XX
PT Identifying agonists and antagonists of tumor necrosis factor related
PT receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of
PT cancer, AIDS, Alzheimer's disease, bone disease etc.
XX
PS Disclosure; Page 12-13; 23pp; English.
XX
CC The present sequence represents tumour necrosis factor receptor (TNFR)
CC TR31, also known as DR3, Apo3, WSL-1 or LARD. The invention relates to
CC TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and their
CC ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in claimed
CC methods of identifying agonists and antagonists, i.e. compounds that bind

CC to the receptors or ligand, and which activate (agonist) or inhibit
CC activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for
CC identifying agonists, antagonists, ligands, receptors, substrates,
CC enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The
CC agonists and antagonists are useful for treatment of chronic and acute
CC inflammation, arthritis, septicaemia, autoimmune disease e.g.
CC inflammatory bowel disease, psoriasis, transplant rejection, graft versus
CC host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
CC lymphoproliferative disorders), atherosclerosis, Alzheimer's disease,
CC etc., caused by imbalance of TR1, TR3, TR5 or TL3
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDPTFLAWENHNHNSCARCQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGCLPGFYEHGDCVSCP 180
Db 121 WFVECOVSQCVSSSPFYCQPCDCLGALHHRHRLTLLCSRRDTCGCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADDEAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCWPHKPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTWPGYPETQEALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTWPGYPETQEALCPQVTSW 300
Qy 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQQPAGLGAVVAALERMGLDGCVEDLRSRLQRP 417

RESULT 6
AAB36265
ID AAB36265 standard; protein; 417 AA.
XX
AC AAB36265;
XX
DT 20-FEB-2001 (first entry)
XX
DE Human death domain containing receptor DR3.
XX
KW Human; death domain containing receptor; DR3; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
PD 02-NOV-2000.
XX
PF 21-APR-2000; 2000WO-US010741.
XX
PR 22-APR-1999; 99US-0130488P.
XX
PR 28-MAY-1999; 99US-0136741P.
XX
FA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
XX WPI; 2000-687263/67.
DR N-PSDB; AAC68777.
XX
XX Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent.
XX
XX Claim 1; Fig 2; 273pp; English.
XX
XX The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing
XX
XX Sequence 417 AA;
XX
Query Match 100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
Qy 121 WFVECOVSQCSSSPFYCQPCDCLDGCALHRRHRLTLCRRDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVECOVSQCSSSPFYCQPCDCLDGCALHRRHRLTLCRRDTCGTCPLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300
Qy 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTTLGLRAE 360
Db 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTTLGLRAE 360
Qy 361 IEAVEVEIGRFDDQOYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDDQOYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417
RESULT 7
AAB97370
ID AAB97370 standard; protein; 417 AA.
XX
AC AAB97370;
XX
XX 15-AUG-2001 (first entry)
XX
XX Human rheumatoid arthritis associated transmembrane protein.
XX

Rheumatoid arthritis; transmembrane protein; human.
Homo sapiens.
WO200132921-A2.
XX
PD 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-JP007690.
XX
XX 01-NOV-1999; 99JP-00310805.
XX
XX (SHIO/) SHIOZAWA S.
XX
XX Shiozawa S, Konishi Y;
XX
XX WPI; 2001-308750/32.
DR N-PSDB; AAH27782.
XX
XX Diagnosing rheumatoid arthritis by probing digested human genomic DNA or
PT comparing expression of mRNA or polypeptide of a region of transmembrane
PT protein.
XX
XX Disclosure; Page 15-17; 21pp; Japanese.
XX
XX This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridising it
CC with a probe for the DNA encoding the present protein which is a
CC rheumatoid arthritis associated transmembrane protein. The method is used
CC for the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments
XX
XX Sequence 417 AA;
XX
Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
Qy 121 WFVECOVSQCSSSPFYCQPCDCLDGCALHRRHRLTLCRRDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVECOVSQCSSSPFYCQPCDCLDGCALHRRHRLTLCRRDTCGTCPLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYYRHCHWPKPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTSW 300
Qy 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTTLGLRAE 360
Db 301 DOLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTTLGLRAE 360
Qy 361 IEAVEVEIGRFDDQOYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDDQOYEMLKRWROQOPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417
RESULT 8
AAO17879
ID AAO17879 standard; protein; 417 AA.
XX
AC AAO17879;
XX

DT 22-AUG-2002 (first entry)
XX Human rheumatoid arthritis associated DR3 gene related protein #1.
DE Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy.
XX
OS Homo sapiens.
XX WO200234912-A1.
FN 02-MAY-2002.
XX 24-OCT-2001; 2001WO-JP009313.
XX 24-OCT-2000; 2000JP-00324296.
PR 27-MAR-2001; 2001JP-00090546.
PR 30-MAR-2001; 2001JP-00099990.
XX (NEWI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX Shiozawa S, Konishi Y;
FI WPI; 2002-417132/44.
DR N-PSDB; AAL47186.
XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies.
XX
PS Claim 2; Page 69-70; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a protein described in the exemplification of the invention
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNETCLVCPQDTFLAWENHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNETCLVCPQDTFLAWENHNSCARCOACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVEQVQSVCSSSPFYQCPCLDCGALHRRHRLTLLCSRDTCGTLPGFYEHGDCVSCP 180
Db 121 WFVEQVQSVCSSSPFYQCPCLDCGALHRRHRLTLLCSRDTCGTLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRFQVLLAGLVPLLLGATLTYTYRHCHWPKPIYTADEAG 240
Db 181 TSTLGSCPERCAAVCGWRFQVLLAGLVPLLLGATLTYTYRHCHWPKPIYTADEAG 240

Qy 241 MEALTTPPPATHSLPDSAHITLLAPPDSEKICTVQLVGNSTWPGVPETOALCPQVTSW 300
Db 241 MEALTTPPPATHSLPDSAHITLLAPPDSEKICTVQLVGNSTWPGVPETOALCPQVTSW 300

Qy 301 DQLPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYVMDVAVPARRWKFEVRTILGLREAE 360
Db 301 DQLPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYVMDVAVPARRWKFEVRTILGLREAE 360

Qy 361 LEAVEVEIGREFDQOYEMLKEWROOQAPGLGAVNVAALERMGLDGCVEDLRSRLQRP 417
Db 361 LEAVEVEIGREFDQOYEMLKEWROOQAPGLGAVNVAALERMGLDGCVEDLRSRLQRP 417

RESULT 9
AAU86139
ID AAU86139 standard; protein; 417 AA.
XX
AC AAU86139;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
KW neuroprotective.
XX
OS Homo sapiens.
XX WO200153486-A1.
FN
XX 26-JUL-2001.
XX
XX 11-FEB-2000; 2000WO-US003565.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 11-MAR-1999; 99US-0123972P.
PR 11-MAY-1999; 99US-0133459P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 22-JUN-1999; 99US-0140653P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149395P.
PR 31-AUG-1999; 99US-0151689P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 05-JAN-2000; 2000WO-US000219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
XX Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
XX Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
DR N-PSDB; ABK40265.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT benign or malignant tumors, leukemias and lymphoid malignancies,
PT inflammatory, angiogenic and immunologic disorders.
XX
XX Claim 61; Fig 24; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The PRO
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC treating benign or malignant tumours (e.g. renal, kidney, bladder,
CC breast, etc), leukaemias and lymphoid malignancies, other disorders such
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC stromal and blastocoelec disorders, inflammatory, immune, and angiogenic
CC disorders. The polynucleotide sequences are also useful in gene therapy.
CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYTRHCHWPHKPLVTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYTRHCHWPHKPLVTADAG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLGNSWTPGYPETQEQALCPQVTSW 300
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLGNSWTPGYPETQEQALCPQVTSW 300
QY 301 DQLPSRALGPAAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSRALGPAAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKWROQOQAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKWROQOQAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 10

ABG73993
ID ABG73993 standard; protein; 417 AA.

XX AC ABG73993;

XX DT 01-APR-2003 (first entry)

XX DE Human Apo3 protein.

XX KW APO-3; human; apoptosis; monoclonal antibody; cytostatic; cancer;
XX autoimmune; inflammatory; neurodegenerative disease.

XX OS Homo sapiens.

XX FH Location/Qualifiers
XX FT Peptide 1..24
XX FT Domain /label= signal_peptide
XX FT Modified-site 25..198 /note= "Extracellular domain"
XX FT Modified-site 67 /note= "N glycosylated"
XX FT Modified-site 106 /note= "N glycosylated"
XX FT Domain 199..224 /note= "Transmembrane domain"
XX FT Domain 225..417 /note= "Intracellular domain"
XX FT Region 236 /note= "This Alanine is not present in the Apo3 variant that is expressed in foetal heart"

XX US6469144-B1.

XX PD 22-OCT-2002.

XX PF 31-MAR-1997; 97US-00828683.

XX PR 01-APR-1996; 96US-00625328.

XX PR 23-SEP-1996; 96US-00710802.

XX PA (GETH) GENENTECH INC.

XX PA Ashkenazi AJ;

XX WPI; 2003-147110/14.
XX DR N-PSDB; ABX15842.
XX Novel isolated monoclonal antibody useful for activating or stimulating
XX apoptosis in cancer cells, comprises an antigen binding site which binds
XX to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.
XX Claim 1; Fig 4; 48pp; English.

XX This invention relates to an isolated monoclonal antibody comprising an
XX antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI)
XX polypeptide and an antibody that binds the Apo3 protein. The antibodies
XX of the invention may have cytostatic activity and may act as activators
XX or stimulator of apoptosis in cancer cells, as blockers of excessive
XX apoptosis or of the autoimmune/inflammatory effects of Apo-3 resulting
XX from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase
XX (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in
XX therapeutic purposes for activating or stimulating apoptosis in cancer
XX cells and may be used to block excessive apoptosis (for example in
XX neurodegenerative disease), or to block potential autoimmune/
XX inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB
XX activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody
XX may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g.
XX detecting Apo-2LI or Apo-3 expression in specific cells, tissues or
XX serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant
XX cell culture or natural sources. The present sequence represents the
XX human Apo3 protein which was used to generate the antibody of the
XX invention

XX SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVEQCVSQVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYTRHCHWPHKPLVTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYTRHCHWPHKPLVTADAG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVOLGNSWTPGYPETQEQALCPQVTSW 300
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DB 301 DQLPSRALGPAAAPTLSPESAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKWROQOQAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKWROQOQAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 11

ABU08252
ID ABU08252 standard; protein; 417 AA.

XX AC ABU08252;

XX DT 13-MAY-2003 (first entry)

XX XX

DE Human Apo-3 protein.
XX
KW Human; Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; AIDS;
KW acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer;
KW Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis;
KW retinitis pigmentosa; aplastic anaemia; cerebellar degeneration;
KW myocardial infarction; reperfusion injury; toxin-induced liver disease;
KW chromosome 1q36.3; programmed cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..198
FT /label= Extracellular domain
FT /note= "This domain is claimed in claim 26"
FT Domain 338..417
FT /label= Death domain
FT /note= "This domain is claimed in claim 27"
XX
PN US2002165157-A1.
XX
PD 07-NOV-2002.
XX
XX 21-FEB-2002; 2002US-00081280.
XX
PR 01-APR-1996; 96US-0014699P.
PR 23-SEP-1996; 96US-0036943P.
PR 31-MAR-1997; 97US-00829270.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ;
XX
XX WPI, 2003-298703/29.
DR N-PSDB; ABX13179.
XX
FT New biologically active Apo-2LI or Apo-3 polypeptide, useful for
FT preparing a composition for treating cancer.
XX
PS Claim 22; Fig 4; 45pp; English.
XX
CC The invention relates to an new isolated biologically active Apo-2LI or
CC Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI
CC or Apo-3 appearing as ABU08251 and ABU08252. Also included are a
CC chimaeric molecule comprising the Apo-2LI fused to a heterologous amino
CC acid sequence; a dimer molecule comprising a first Apo-2LI and a second
CC Apo-2LI, an antibody that binds to Apo-2LI or Apo-3 (or to its
CC extracellular domain sequence), an isolated nucleic acid encoding Apo-2LI
CC or Apo-3, a vector comprising the nucleic acid, a host cell comprising
CC the vector, a method of producing Apo-2LI and a non-human (transgenic or
CC knockout) animal that contains cells that express nucleic acid encoding
CC Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3
CC are involved in apoptosis (programmed cell death) which is implicated in
CC AIDS, (acquired immunodeficiency syndrome), stroke, Alzheimer's disease,
CC Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis,
CC retinitis pigmentosa, aplastic anaemia, cerebellar degeneration,
CC myocardial infarction, reperfusion injury and toxin-induced liver
CC diseases. The gene for both proteins is located on chromosome 1q36.3 Apo-
CC 2LI and Apo-3 are also useful for preparing a composition for treating
CC cancer. The present sequence represents Apo-3
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAAAVALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAAVALLVLLGARAGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARQCACDEQASQVALENCASAVADTRCGCKPG 120
|||||

Db 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARQCACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVQSVSSPPFFCQPCDCLCGALHRRHTRLLCSRDDTDCGTCLPGFYEHGDCVSCP 180
|||
Db 121 WFVECVQSVSSPPFFCQPCDCLCGALHRRHTRLLCSRDDTDCGTCLPGFYEHGDCVSCP 180
|||
QY 181 TSTLGSCPERCAAVCGWRQFVVOVLLAGLVVPLLGLATLTYYRHCHWPHKPLVTADDEAG 240
|||
Db 181 TSTLGSCPERCAAVCGWRQFVVOVLLAGLVVPLLGLATLTYYRHCHWPHKPLVTADDEAG 240
|||
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNSSWTPGYPETQEALCPQVTWSW 300
|||
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNSSWTPGYPETQEALCPQVTWSW 300
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QY 301 DQLPSRALGPAAATLSPSPAGSPANMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
|||
Db 301 DQLPSRALGPAAATLSPSPAGSPANMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
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QY 361 IEAVEVEIGRFDQOQYEMLKRWROQQPAGLCAGVAAALERMGLDGCVEDLSRLQGP 417
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Db 361 IEAVEVEIGRFDQOQYEMLKRWROQQPAGLCAGVAAALERMGLDGCVEDLSRLQGP 417
|||
RESULT 12
ABG73859
ID ABG73859 standard; protein; 417 AA.
XX
AC ABG73859;
XX
DT 03-APR-2003 (first entry)
XX
DE Human foetal heart Apo-3 protein.
XX
KW Human; Apo-3; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
KW nuclear factor-kappa B; NF-kappa B; Alzheimer's disease; AIDS;
KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;
KW Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis;
KW retinitis pigmentosa; cerebellar degeneration; aplastic anaemia;
KW myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; cancer; lupus; herpes virus infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..198
FT /note= "Extracellular domain. This domain is
FT specifically claimed in claim 2 of the specification"
FT Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..417
FT /note= "Mature Apo-3 protein"
FT Modified-site 67
FT /note= "N-glycosylated"
FT Modified-site 106
FT /note= "Transmembrane domain"
FT Domain 199..224
FT /note= "Transmembrane domain"
FT Domain 225..417
FT /note= "Intracellular domain"
FT Domain 338..417
FT /note= "Death domain. This domain is specifically
FT claimed in claim 3 of the specification"
XX
PN US6462176-B1.
XX
PD 08-OCT-2002.
XX
PF 11-SEP-1997; 97US-00928069.
XX
PR 23-SEP-1996; 96US-0026943P.
XX
FA (GETH) GENENTECH INC.
XX

OY 361 IEAVEVEIGRFRDQOQYEMLKRWQOQAPAGLVAAALERMGLDGCVEDLRSRLQGRP 417
 Db 361 IEAVEVEIGRFRDQOQYEMLKRWQOQAPAGLVAAALERMGLDGCVEDLRSRLQGRP 417

RESULT 15
 ABG73824
 ID ABG73824 standard; protein; 417 AA.
 AC ABG73824;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE Human apoptotic protein, Apo-3.
 KW human; Apo-2 ligand inhibitor; Apo-2LI; apoptosis; NF-kappaB; JNK;
 KW c-Jun N-terminal kinase; necrosis factor kappa B; chimeric molecule;
 KW tissue-specific typing; Apo-3; transgenic; affinity purification;
 KW competitive-type receptor binding assay.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..198 /label= Extracellular_domain
 FT Protein 1..181 /label= Apo-2LI
 FT /note= "Specifically claimed in claim 4. Residues 1-181
 of Apo-3 represent Apo2LI"
 FT Domain 34..71 /label= Cysteine-rich_domain_1
 FT Domain 72..115 /label= Cysteine-rich_domain_2
 FT Domain 116..163 /label= Cysteine-rich_domain_3
 FT Domain 164..181 /label= Cysteine-rich_domain_4
 FT /note= "This cysteine-rich domain is apparently truncated
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 FT Domain 338..417 /label= Death_domain
 FT
 XX US2002146768-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 19-NOV-2001; 2001US-009393234.
 XX
 PR 01-APR-1996; 96US-00625328.
 PR 23-SEP-1996; 96US-00710802.
 PR 31-MAR-1997; 97US-00828683.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ;
 XX
 DR WPI; 2003-174176/17.
 DR N-PSDB; ABX15507, ABX15003.
 XX
 FT New isolated biologically active Apo-2LI or Apo-3 used to induce
 FT apoptosis in mammalian cells.
 XX
 PS Claim 22; Fig 4; 44pp; English.
 XX
 CC The invention relates to an isolated biologically active Apo-2LI or Apo-3
 CC which has at least 80% sequence identity with native sequence Apo-2LI
 CC having 1-181 amino acids or Apo-3 having 1-417 amino acids, respectively.
 CC Apo-3 can be employed therapeutically to induce apoptosis or NF-kappaB or
 CC JNK mediated gene expression in mammalian cells. The Apo-3 chimeric
 CC molecules can be employed therapeutically to inhibit apoptosis; necrosis
 CC factor (NF)-kappaB induction; c-Jun N-terminal kinase (JNK) activation.
 CC Apo-2LI can be employed therapeutically to inhibit mammalian cell

CC apoptosis in vivo or ex vivo. Nucleic acid sequences encoding the Apo-3
 CC or Apo-2LI may be used as a diagnostic for tissue-specific typing. The
 CC isolated Apo-3 or Apo-2LI may be used in quantitative diagnostic assays
 CC as a control against which samples containing unknown quantities of Apo-3
 CC or Apo-2LI may be prepared. Apo-3 preparations are also useful in
 CC generating antibodies, as standards in assays for Apo-3 or Apo-2LI, in
 CC affinity purification techniques, and in competitive-type receptor
 CC binding assays when labelled with, e.g. radioiodine, enzymes, or
 CC fluorophores. Modified forms of the Apo-3, e.g. Apo-3-IGG chimeric
 CC molecules can be used as immunogens in producing anti-Apo-3 antibodies.
 CC Nucleic acids which encode Apo-3 or its modified forms can also be used
 CC to generate either transgenic animals or knock out animals, e.g. mouse or
 CC rat, which, in turn, are useful in the development and screening of
 CC therapeutically useful reagents. The Apo-3 polypeptide stimulates or
 CC induces apoptotic activity in mammalian cells. The present sequence
 CC represents the human apoptotic protein, Apo-3. Residues 1-181 of Apo3
 CC represent Apo2LI which may be a secreted or soluble form of Apo3
 XX Sequence 417 AA;
 SQ

Query Match 100.0%; Score 2323; DB 6; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.3e-161;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
 Db 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60

OY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
 Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120

OY 121 WFVECVSQSVSSPFYCQCLDCGALHRLHRLTLCSRRDTCGTCLPGFYEHGDCVSCP 180
 Db 121 WFVECVSQSVSSPFYCQCLDCGALHRLHRLTLCSRRDTCGTCLPGFYEHGDCVSCP 180

OY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYTRHCWPHKPLVTADAG 240
 Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYTRHCWPHKPLVTADAG 240

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 Db 241 MEALTTPPATHLSPLDSANTLLAPPDSSEKICTVOLGNSWTPGYPETOALCPQVTWSW 300

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 Db 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360

OY 361 IEAVEVEIGRFRDQOQYEMLKRWQOQAPAGLVAAALERMGLDGCVEDLRSRLQGRP 417
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Search completed: June 27, 2005, 13:43:35
 Job time : 167 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:40:47 ; Search time 161 Seconds
(without alignments)

996.003 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2323	100.0	417	9	US-09-874-138-5
3	2323	100.0	417	9	US-09-993-234-6
4	2323	100.0	417	10	US-09-314-889-4
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9	2323	100.0	417	14	US-10-175-902-5
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12	2323	100.0	417	14	US-10-211-884-24
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14	2323	100.0	417	15	US-10-211-858-24
15	2323	100.0	417	15	US-10-415-247-3
16	2323	100.0	417	16	US-10-648-825-5
17	2323	100.0	417	16	US-10-774-622-5
18	2323	100.0	417	16	US-10-744-379-2
19	2323	100.0	833	14	US-10-226-296-5
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26	1404	60.4	411	16	US-10-744-379-6
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36	387.5	16.7	471	9	US-09-970-532-2
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ALIGNMENTS

RESULT 1
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; Sequence 4, Application US/09333966
; Patent No. US20020009773A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-333-966-4

Query Match      100.0%; Score 2323; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db      1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
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Db      241 MEALTPPPATHSLPDSAHNTLLAPPDSSEKICTVOLVGNSTWPGYPETQALCPQVTSW 300
Qy      301 DQPSRALGPAAPTLPSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db      301 DQPSRALGPAAPTLPSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Qy      361 IEAVEVEIGRFRDQOQYEMLKRWQOQPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417
Db      361 IEAVEVEIGRFRDQOQYEMLKRWQOQPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 2
US-09-874-138-5
; Sequence 5, Application US/09874138
; Patent No. US20020072031A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/874,138
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
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; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-138-5

Query Match      100.0%; Score 2323; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db      1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy      61 CTEPCGNSCLVCPQDTFLAWENHNHSECCARQACDEQASQVALENCASAVADTRCGCKPG 120
Db      61 CTEPCGNSCLVCPQDTFLAWENHNHSECCARQACDEQASQVALENCASAVADTRCGCKPG 120
Qy      121 WFVECOVSQCVSSPPFYCQPCDCLCGALHRRHRLICSRDDTCGCLPGFYEHGDCVSCP 180
Db      121 WFVECOVSQCVSSPPFYCQPCDCLCGALHRRHRLICSRDDTCGCLPGFYEHGDCVSCP 180
Qy      181 TSTLGSCPERCAAVCGWRQFWQVLLAGLVPLLLGATLTYTYRHCHWPKPLVTAD EAG 240
Db      181 TSTLGSCPERCAAVCGWRQFWQVLLAGLVPLLLGATLTYTYRHCHWPKPLVTAD EAG 240
Qy      241 MEALTPPPATHSLPDSAHNTLLAPPDSSEKICTVOLVGNSTWPGYPETQALCPQVTSW 300
Db      241 MEALTPPPATHSLPDSAHNTLLAPPDSSEKICTVOLVGNSTWPGYPETQALCPQVTSW 300
Qy      301 DQPSRALGPAAPTLPSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db      301 DQPSRALGPAAPTLPSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Qy      361 IEAVEVEIGRFRDQOQYEMLKRWQOQPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417
Db      361 IEAVEVEIGRFRDQOQYEMLKRWQOQPAGLGAVVAAALERMGLDGCVEDLRSRLQRP 417

RESULT 3
US-09-993-234-6
; Sequence 6, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-993-234-6

Query Match      100.0%; Score 2323; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120

Qy 121 WFVEQVQSVSSPFYCPQCLDCGALHRRTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVEQVQSVSSPFYCPQCLDCGALHRRTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAACVGRQWQVQVLLAGLVVPLLGLATLTYTRHCPHPKPLVTADAG 240
Db 181 TSTLGSCPERCAACVGRQWQVQVLLAGLVVPLLGLATLTYTRHCPHPKPLVTADAG 240

Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTWTPGYPTQEALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTWTPGYPTQEALCPQVTSW 300

Qy 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYVMDAVPARRWKEFVRTLGLREAE 360

Qy 361 IEAVEVEIGRFDQOQYEMLKRWQOQAGLGAVAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDQOQYEMLKRWQOQAGLGAVAALERMGLDGCVEDLRSRLQRP 417

RESULT 4
US-09-314-889-4
; Sequence 4, Application US/09314889
; Publication No. US20030077694A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/815,469
; FILING DATE:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-314-889-4

Query Match      100.0%; Score 2323; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120

Qy 121 WFVEQVQSVSSPFYCPQCLDCGALHRRTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
Db 121 WFVEQVQSVSSPFYCPQCLDCGALHRRTRLLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAACVGRQWQVQVLLAGLVVPLLGLATLTYTRHCPHPKPLVTADAG 240
Db 181 TSTLGSCPERCAACVGRQWQVQVLLAGLVVPLLGLATLTYTRHCPHPKPLVTADAG 240

Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTWTPGYPTQEALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVOLVGNSTWTPGYPTQEALCPQVTSW 300

Qy 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYVMDAVPARRWKEFVRTLGLREAE 360

Qy 361 IEAVEVEIGRFDQOQYEMLKRWQOQAGLGAVAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFDQOQYEMLKRWQOQAGLGAVAALERMGLDGCVEDLRSRLQRP 417

RESULT 5
US-10-005-842-5
; Sequence 5, Application US/10005842
; Publication No. US20020098550A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Su, Jeffrey
; APPLICANT: Rosen, Craig A.
```

TITLE OF INVENTION: Death Domain Containing Receptor 5
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,583
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/040,846
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
TELEFAX: 3013098439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-005-842-5

Query Match 100.0%; Score 2323; DB 13; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQRPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSQVSSPFFYCPCLDCGALHRRHRLLCSSRDTCGCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSQVSSPFFYCPCLDCGALHRRHRLLCSSRDTCGCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD 240
Qy 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTWSW 300
Qy 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMQAVPARRWKEFVRTILGLREAE 360
Db 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMQAVPARRWKEFVRTILGLREAE 360
Qy 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417

RESULT 6
US-10-081-280-6
Sequence 6, Application US/10081280
Publication No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-081-280-6

Query Match 100.0%; Score 2323; DB 13; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQRPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSQVSSPFFYCPCLDCGALHRRHRLLCSSRDTCGCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSQVSSPFFYCPCLDCGALHRRHRLLCSSRDTCGCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTAD 240
Qy 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHILLAPPDSSEKICTVOLVGNSTPGYPETQEALCPQVTWSW 300
Qy 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMQAVPARRWKEFVRTILGLREAE 360
Db 301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMQAVPARRWKEFVRTILGLREAE 360
Qy 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGRFDOQYEMLKWROQQPAGLGAVVAALERMGLDGCVEDLRSRLQGP 417

Db 361 IEAVEVEIGRFDQOYEMLKRWROQOPAGLGAHVAAALERMGLDGCVEDLRSRLORGP 417

US-10-112-793-6

RESULT 7

Sequence 6, Application US/10112793

Publication No. US20020192729A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,793

FILING DATE: 28-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997

APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996

APPLICATION NUMBER: 08/710802

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 417 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-112-793-6

Query Match 100.0%; Score 2323; DB 13; Length 417;

Best Local Similarity 100.0%; Pred. No. 5.3e-163;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCACAGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCACAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCASAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSVSSSPFYCPCLDCGALHRRHLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Db 121 WFVECVQSVSSSPFYCPCLDCGALHRRHLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADAG 240

Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADAG 240

Qy 241 MEALTPPPATHLSPLDLSAHTLLAPDSEKICTVOLVGNWTPGYPETQEALCPQVTSW 300

Db 241 MEALTPPPATHLSPLDLSAHTLLAPDSEKICTVOLVGNWTPGYPETQEALCPQVTSW 300

Qy 301 DQLPSRALGPAAAPTSLSPSPAGSPAMMLOPGLYDVMADVAPARRWKEFVRTLGLREAE 360

Db 301 DQLPSRALGPAAAPTSLSPSPAGSPAMMLOPGLYDVMADVAPARRWKEFVRTLGLREAE 360

Qy 361 IEAVEVEIGRFDQOYEMLKRWROQOPAGLGAHVAAALERMGLDGCVEDLRSRLORGP 417

Db 361 IEAVEVEIGRFDQOYEMLKRWROQOPAGLGAHVAAALERMGLDGCVEDLRSRLORGP 417

RESULT 8

US-10-112-193-10

Sequence 10, Application US/10112193

Publication No. US20030004313A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,193

FILING DATE: 28-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069

FILING DATE: 11-Sep-1997

APPLICATION NUMBER: 60/026943

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1052R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 417 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-112-193-10

Query Match 100.0%; Score 2323; DB 14; Length 417;

Best Local Similarity 100.0%; Pred. No. 5.3e-163;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCACAGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCACAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCASAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSVSSSPFYCPCLDCGALHRRHLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Db 121 WFVECVQSVSSSPFYCPCLDCGALHRRHLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADAG 240

Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPHKPLVTADAG 240

Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSWTPGYPETOALCPQVWTSW 300
Db |||||
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSWTPGYPETOALCPQVWTSW 300
Db |||||
Qy 301 DQLPSRALGPAAPPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db |||||
Qy 301 DQLPSRALGPAAPPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db |||||
Qy 361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417
Db |||||
361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417
RESULT 9
US-10-175-902-5
; Sequence 5, Application US/10175902
; Publication No. US20030108516A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/10175,902
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-902-5

Query Match 100.0%; Score 2323; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db |||||
Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db |||||
Qy 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120
Db |||||
Qy 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120
Db |||||
Qy 121 WFVECVQSVCSVSSPPFCQCLDCGALHRRHTRLLCSRRTDCGTCCLPGFYEHGDCVSCP 180
Db |||||
Qy 121 WFVECVQSVCSVSSPPFCQCLDCGALHRRHTRLLCSRRTDCGTCCLPGFYEHGDCVSCP 180
Db |||||
Qy 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTADBEAG 240
Db |||||
Qy 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTADBEAG 240
Db |||||
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSWTPGYPETOALCPQVWTSW 300
Db |||||
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSWTPGYPETOALCPQVWTSW 300
Db |||||
Qy 301 DQLPSRALGPAAPPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db |||||
Qy 301 DQLPSRALGPAAPPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db |||||

Qy 361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417
Db |||||
361 IEAVEVEIGRDOOQYEMLKRWROQOPAGLGAHVAAALERMGLDGCVEDLRSRLQRP 417
RESULT 10
US-10-189-189-4
; Sequence 4, Application US/10189189
; Publication No. US20030170203A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; FILE REFERENCE: 1488.031000C
; CURRENT APPLICATION NUMBER: US/10189,189
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 60/314,314
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/303,155
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 09/557,908
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 60/136,741
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/130,488
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 08/815,469
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: US 60/037,341
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/028,711
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/013,285
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-189-4

Query Match 100.0%; Score 2323; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db |||||
Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db |||||
Qy 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120
Db |||||
Qy 61 CTEPCGNSTCLVCPQDITFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120
Db |||||
Qy 121 WFVECVQSVCSVSSPPFCQCLDCGALHRRHTRLLCSRRTDCGTCCLPGFYEHGDCVSCP 180
Db |||||
Qy 121 WFVECVQSVCSVSSPPFCQCLDCGALHRRHTRLLCSRRTDCGTCCLPGFYEHGDCVSCP 180
Db |||||
Qy 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTADBEAG 240
Db |||||
Qy 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPHKPLVTADBEAG 240
Db |||||
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSWTPGYPETOALCPQVWTSW 300
Db |||||
Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSWTPGYPETOALCPQVWTSW 300
Db |||||
Qy 301 DQLPSRALGPAAPPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db |||||
Qy 301 DQLPSRALGPAAPPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db |||||


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Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
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Db 121 WFVEQVSCVSSSPFFYQCPCLDCGALHRRHRLLCSSRDTCGCLPGFVEHGDGCVSCP 180
Qy 181 TSTLGSQVSCVSSSPFFYQCPCLDCGALHRRHRLLCSSRDTCGCLPGFVEHGDGCVSCP 240
Db 181 TSTLGSQVSCVSSSPFFYQCPCLDCGALHRRHRLLCSSRDTCGCLPGFVEHGDGCVSCP 240
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300
Qy 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417
Db 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417

RESULT 13
US-10-310-793-4
; Sequence 4, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: human
US-10-310-793-4

Query Match 100.0%; Score 2323; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEORPRCAAAVAALLVLGARAQGGTRSPRCDACDGHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVEQVSCVSSSPFFYQCPCLDCGALHRRHRLLCSSRDTCGCLPGFVEHGDGCVSCP 180
Db 121 WFVEQVSCVSSSPFFYQCPCLDCGALHRRHRLLCSSRDTCGCLPGFVEHGDGCVSCP 180
Qy 181 TSTLGSQVSCVSSSPFFYQCPCLDCGALHRRHRLLCSSRDTCGCLPGFVEHGDGCVSCP 240
Db 181 TSTLGSQVSCVSSSPFFYQCPCLDCGALHRRHRLLCSSRDTCGCLPGFVEHGDGCVSCP 240
Qy 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPETQALCPQVTSW 300
Qy 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPQPOLYDMDAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417
Db 361 IEAVEVEIGRDOQYEMLKWROQOQAGLVAVYAAALERMGLDGCVEDLSRLQRP 417

RESULT 14
US-10-211-858-24
; Sequence 24, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
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; SEQ ID NO 24
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-858-24

Query Match      100.0%; Score 2323; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRCGCPAGHYLKAP 60
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Db 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRCGCPAGHYLKAP 60
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Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARQCACDEQASQVALENCSAVADTRCGCKPG 120
    |||
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARQCACDEQASQVALENCSAVADTRCGCKPG 120
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Qy 121 WFVECOVSQCQVSSSPFFYQCPCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
    |||
Db 121 WFVECOVSQCQVSSSPFFYQCPCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
    |||

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCPHKLPLVTAD EAG 240
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Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCPHKLPLVTAD EAG 240
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Qy 241 MEALTPPPATHLSPLDSAHTLLAPDSEKICTVQLVGNNSWTPGYPETQEALCPQVTMSW 300
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Qy 301 DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360
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Db 301 DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360
    |||

Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAPAGLVAVYAAALERMGLDGCVEDLRSRLQRP 417
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RESULT 15
US-10-415-247-3
; Sequence 3, Application US/10415247
; Publication No. US20040013655A1
; GENERAL INFORMATION:
; APPLICANT: Shiozawa, Shunichi
; TITLE OF INVENTION: Genome responsible for chronic rheumatoid arthritis,
; TITLE OF INVENTION: diagnostic method, pathogenicity judging method and
; TITLE OF INVENTION: detection-use diagnostic kit of chronic rheumatoid
; TITLE OF INVENTION: arthritis, and therapeutic method and medicine of
; TITLE OF INVENTION: chronic rheumatoid arthritis
; FILE REFERENCE: TLOP1-2
; CURRENT APPLICATION NUMBER: US/10/415,247
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2000-324296
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: JP 2001-90546
; PRIOR FILING DATE: 2001-3-27
; PRIOR APPLICATION NUMBER: JP 2001-99990
; PRIOR FILING DATE: 2001-3-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-247-3

Query Match      100.0%; Score 2323; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRCGCPAGHYLKAP 60
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Db 1 MEQRPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRCGCPAGHYLKAP 60
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Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARQCACDEQASQVALENCSAVADTRCGCKPG 120
Qy 121 WFVECOVSQCQVSSSPFFYQCPCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 121 WFVECOVSQCQVSSSPFFYQCPCLDCGALHHRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCPHKLPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCPHKLPLVTAD EAG 240
Qy 241 MEALTPPPATHLSPLDSAHTLLAPDSEKICTVQLVGNNSWTPGYPETQEALCPQVTMSW 300
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Db 301 DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAPAGLVAVYAAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAPAGLVAVYAAALERMGLDGCVEDLRSRLQRP 417

Search completed: June 27, 2005, 13:56:23
Job time : 163 secs
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C:Superfamily: chorion class A protein pc292

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Matches 18: Conservative 7; Mismatches 29; Indels 0; Gaps 0;

QY 179 CPTSTLGSPERCAAVC 195
Db 130 C-----GGCGSGCGSSC 141

Db 29 MRSRGQFQVSSSLPDIYCRC-GESGHLAKDCDLQED-----ACYNCGRGGHIAD 79
QY 61 CTEP-----CGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCSSAVADTR 114
Db 80 CKEPKREEQ-----CYNCGKPGHLARDCHDADE-QKCYSCGEFGH--IQDCTKVKCYR 132
QY 115 CGCKPGFWFVEQVQSCVSSSPFYCQPCLDGALHR 149
Db 133 CG-ETGHV-----AINCSKTSEVNCYRCGESGHLAR 162

RESULT 14

I48297
cellular nucleic acid binding protein clone 6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48297; S19861; S19959
R:Warden, C.H.; Krisans, S.K.; Furcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; T
Genomics 24, 14-19, 1994
A:Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identif
A:Reference number: A55499; MUID:95203870; PMID:7896269
A:Accession: I48297
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170 <RES>
A:Cross-references: UNIPROT:P53996; EMBL:Z11870; NID:g50472; PIDN:CAA77896.1; PID:g50473
R:Warden, C.H.
submitted to the EMBL Data Library, January 1992
A:Description: Cellular nucleic acid binding protein (CNBP) is an extremely conserved cy
A:Reference number: S19861
A:Accession: S19861
A:Molecule type: mRNA
A:Residues: 1-170 <WA2>
A:Cross-references: EMBL:X63866; NID:g50470; PIDN:CAA45345.1; PID:g50471
C:Superfamily: cellular nucleic acid-binding protein

Query Match 7.9%; Score 89.5; DB 2; Length 170;
Best Local Similarity 25.2%; Pred. No. 6.2;
Matches 39; Conservative 18; Mismatches 71; Indels 27; Gaps 8;

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Db 29 MRSRGQFQVSSSLPDIYCRC-GESGHLAKDCDLQED-----ACYNCGRGGHIAD 79
QY 61 CTEP-----CGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCSSAVADTR 114
Db 80 CKEPKREEQ-----CYNCGKPGHLARDCHDADE-QKCYSCGEFGH--IQDCTKVKCYR 132
QY 115 CGCKPGFWFVEQVQSCVSSSPFYCQPCLDGALHR 149
Db 133 CG-ETGHV-----AINCSKTSEVNCYRCGESGHLAR 162

RESULT 15

I46412
keratin KAP5.4 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I46412; S34215
R:Jenkins, B.J.; Powell, B.C.
J. Invest. Dermatol. 103, 310-317, 1994
A:Title: Differential expression of genes encoding a cysteine-rich keratin family in the
A:Reference number: I46412; MUID:94358466; PMID:7521375
A:Accession: I46412
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-191 <JEN>
A:Cross-references: UNIPROT:Q28583; EMBL:X73434; NID:g313719; PIDN:CAA51829.1; PID:g3137
C:Genetics:
A:Gene: KRTAP5.4
C:Superfamily: ultra-high-sulfur keratin

Query Match 7.9%; Score 89.5; DB 2; Length 191;
Best Local Similarity 22.3%; Pred. No. 6.7;
Matches 42; Conservative 8; Mismatches 61; Indels 77; Gaps 13;
QY 21 GARAQGGTSPRCDCAGDFHKKIGLFCRG-----CPAGHYLKAPCTEPCGHST--CL 71
Db 63 GCSGCGSGKSGCGCG-----CGSSCCCKPVCCCVFVSCSSCGKGGCGSGSGSGKGGCG 117
QY 72 VCPQDTFLAWENHNSECARCOACDEQASQVALENCSSAVADTRCGCKPGFWFVEQVQSCV 131
Db 118 SC-----GSGKGGCGSGCGGS-----GCGP-----SCCVPVCC 146
QY 132 SSSPFYQPCLDGALHRTLLCSRRTDTCGTCLPGFYEHGDC--VSC--PTSTLGGC 187
Db 147 -----CVPACSCSS-----CGK--GGCGSC-----GCSQSSCCRPCCSQSSC 181
QY 188 PERCAAVC 195
Db 182 ---CVPVC 186

Search completed: June 27, 2005, 14:02:57
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 13:43:43 ; Search time 171 Seconds
(without alignments)

583.950 Million cell updates/sec

Title: US-10-081-280-6_COPY_1_195

Perfect score: 1130

Sequence: 1 MEQRPRCAVAALLLVLL.....CVSPTSTLGCSPERCAAVC 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 635772

Minimum DB seq length: 0

Maximum DB seq length: 195

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	198	17.5	189	2	Q95185	Q95185 felis silve
2	197	17.4	189	2	Q97530	Q97530 canis famil
3	173	15.3	150	2	Q9R230	Q9R230 rattus norv
4	164.5	14.6	176	1	TR23 MOUSE	Q9er63 mus musculu
5	161.5	14.3	130	2	Q9WJ70	Q9mj20 macaca mula
6	157.5	13.9	186	2	Q911R5	Q91lr5 vaccinia vi
7	157.5	13.9	186	2	Q9WJB4	Q9wjB4 vaccinia vi
8	155	13.7	186	2	Q9YPR7	Q9y735 cowpox viru
9	153.5	13.6	186	2	Q9YPR7	Q9yp87 cowpox viru
10	146.5	13.0	146	2	Q7Z2V4	Q7zzy4 gallus gall
11	137.5	12.2	169	2	Q9TK60	Q9jke0 rattus norv
12	135.5	11.8	124	2	Q8QS51	Q8sq51 felis silve
13	133.5	11.8	147	2	Q8SQ52	Q8sq52 felis silve
14	132	11.7	117	2	Q6VZR1	Q6vzr1 canarypox v
15	128	11.3	176	2	Q9PZS2	Q9pzs2 human cytom
16	126.5	11.2	65	2	Q8SQ49	Q8sq49 felis silve
17	125	11.1	110	2	Q9BIR2	Q9bir2 paramecium
18	124	11.0	110	2	Q9BIR3	Q9bir3 paramecium
19	123	10.9	167	2	Q8BDC5	Q8bdc5 human cytom
20	123	10.9	176	2	Q91IR3	Q91ir3 human cytom
21	123	10.9	176	2	Q9PZS1	Q9pzs1 human cytom
22	123	10.9	176	2	Q9PZS3	Q9pzs3 human cytom
23	122	10.8	176	2	Q910W9	Q910w9 human cytom
24	122	10.8	176	2	Q91IR4	Q91ir4 human cytom
25	122	10.8	176	2	Q9PZS5	Q9pzs5 human cytom
26	121.5	10.8	172	2	Q91IR0	Q91ir0 human cytom
27	119	10.5	151	2	Q6P2H9	Q6p2h9 homo sapien
28	115	10.2	175	2	Q9PZR6	Q9pze6 human cytom
29	114	10.1	194	2	Q7PI78	Q7pi78 anopheles g
30	113.5	10.0	175	2	Q9PZS5	Q9pzs5 human cytom
31	113	10.0	195	2	Q9D141	Q9d141 mus musculu

32	112	9.9	175	2	Q9PWX3	Q9pxw3 human cytom
33	112	9.9	175	2	Q9PZS8	Q9pzs8 human cytom
34	111.5	9.9	166	2	Q8BDC6	Q8bdc6 human cytom
35	111.5	9.9	175	2	Q910H9	Q910h9 human cytom
36	111.5	9.9	175	2	Q6SWR4	Q6swr4 human cytom
37	111.5	9.9	175	2	Q6SWX0	Q6swx0 human cytom
38	111.5	9.9	175	2	Q9PWY0	Q9pwy0 human cytom
39	111.5	9.9	175	2	Q9PFX94	Q9px94 human cytom
40	111.5	9.9	175	2	Q9PXA1	Q9pxa1 human cytom
41	111.5	9.9	175	2	Q9PZR0	Q9pzo0 human cytom
42	111.5	9.9	175	2	Q9PZR4	Q9pze4 human cytom
43	111.5	9.9	175	2	Q9PZR7	Q9pze7 human cytom
44	111.5	9.9	175	2	Q9PZS6	Q9pzs6 human cytom
45	111.5	9.9	175	2	Q9PZS7	Q9pzs7 human cytom

ALIGNMENTS

RESULT 1

Q95185 ID Q95185 PRELIMINARY; PRT; 189 AA.
AC Q95185;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tumour necrosis factor receptor p60 (Fragment).
GN Name=TNFR-1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OC NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Duthie S., Nasir L., Eckersall P.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -;
DR HSSP; P19438; 1EXT.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 17.5%; Score 198; DB 2; Length 189;

Best Local Similarity 29.4%; Pred. No. 5.3e-09; Mismatches 90; Indels 16; Gaps 4;

Matches 52; Conservative 19; Mismatches 90; Indels 16; Gaps 4;

Qy 11 VAAALLLVLLGARAQG-----GTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCT 62

Db 14 VLLALLVEIYELRVTLGLVPLHLDREKRAIPCPQGYIHPQDINSICCTCKHGKTYLNDCE 73

Qy 63 BPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCASAVADTRCGCKPGWF 122

Db 74 GPGIDTDCRENGTFTASENYLR-QCLSCSKCKEMYQVEISPTVYRDVCGCKRN-- 130

Qy 123 VECQVSCQVSSPFVCPCLDCGALHRRHRLCLSRDDTCGTCPLPGFVHEHGDGCVSC 179

Db 131 ---QRYIYWSETHFOCLNCSLC--LNGTVQISCKETQNTVCTCHAGFFLRNECVSC 182

RESULT 2

Q97530 ID Q97530 PRELIMINARY; PRT; 189 AA.

AC Q97530;

```
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tumor necrosis factor receptor p60 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=21109092; PubMed=1182158; DOI=10.1016/S0165-2427(00)00261-0;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL Vet. Immunol. Immunopathol. 78:207-214(2001).
DR EMBL; AF013955; AAD01516.1; -.
DR HSP; P19438; 1TNR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000345; Cytc heme_BS.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON TER 189
SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;

Query Match 17.4%; Score 197; DB 2; Length 189;
Best Local Similarity 28.6%; Pred.No. 6.5e-09;
Matches 52; Conservative 17; Mismatches 87; Indels 26; Gaps 5;

Qy 11 VAAALLVLLGARAQGQGTGSPR-----CDCAGDFHKIKGLPCCRCGCPAGHYLKAPCT 62
Db 14 VLLALLLEIPISTALVPHPRNRVKRAILCPQGIYIHPQDDSICTCKHGTYLYNDP 73
Qy 63 EPCNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCSAVADTRCGCKPG-- 120
Db 74 GPGLDTCRECENGTFTASENHLR-QCLSCSKCKEMNQVEISPTVYRDTVCGCRKNQY 132
Qy 121 ---WFVECVQSVSSPFYQCPCLDCGALHRRHLLCSRRDTCGCLPGFYEHGDCV 177
Db 133 RFYV-----SETLFCQNCSLC--LNGTVQISQEKQNTICTCHAGFFLREHECV 180
Qy 178 SC 179
Db 181 SC 182

RESULT 3
ID Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Fas receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Corpus luteum;
RA Lareu R.R., Dharmarajan A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104034; AAD20221.1; -.
DR HSP; O92956; lUMA.
DR GO; GO:0016020; C:membrane; IEA.
```

```
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;

Query Match 15.3%; Score 173; DB 2; Length 150;
Best Local Similarity 28.9%; Pred.No. 5.5e-07;
Matches 43; Conservative 16; Mismatches 66; Indels 24; Gaps 5;

Qy 13 AALLVLLG-----ARAQG-----GTRSPRCDGDFHKIKGLPCCRCGCPAGHY 56
Db 1 AVLPLVLGAPELNVRMQGTDISIEGLKRSVRETDNNSEGLY-QVGPFCQCPQGER 59
Qy 57 LKAPCTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCSAVADTRCG 116
Db 60 KVXDCTTSGGAPICHPTCEGEYTDKHYSDKRCRCAFCDEGHGCGLEVTNCTRTQNTKCR 119
Qy 117 CKPGWFVECVQSVSSPFYQCPCLDCG 145
Db 120 CKENFY--CNASLC-----DHCYHCTSCG 141

RESULT 4
TR23 MOUSE
ID TR23 MOUSE STANDARD; PRT; 176 AA.
AC Q9ER63; Q8VHC0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 23 precursor (Tumor
DE necrosis factor receptor p60 homolog 1) (TNF receptor family member
DE SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).
GN Name=Tnfrsf23; Synonyms=Dctrailr1, Tnfrh1, Tnfrsf1a1;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Embryonic stem cells;
RX MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region;
RT implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
RN [2]
RN SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE
RC MODELING OF 52-160.
RC STRAIN=C57BL/6;
RX PubMed=12466268; DOI=10.1074/jbc.M210783200;
RA Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,
RA Gong D., Dobies M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,
RA Burkly L.C., Tschopp J., Zheng T.S.;
RT "Identification of a new murine tumor necrosis factor receptor locus
RT that contains two novel murine receptors for tumor necrosis factor-
RL J. Biol. Chem. 278:5444-5454(2003).
RN [3]
RN SEQUENCE FROM N.A.
RP Pan G., Mao W., Rissler P.;
RT "Characterization of SOB, a member of the TNFR family.";
```

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a cytoplasmic death domain and hence is not capable of inducing apoptosis. May protect cells against TRAIL mediated apoptosis through ligand competition. Cannot induce the NF-kappa-B pathway.
-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-1- TISSUE SPECIFICITY: Ubiquitous.
-1- SIMILARITY: Contains 3 TNFR-Cys repeats.

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EMBL; AJ278264; CAC16405.1; -
EMBL; AJ276505; CAC27352.1; -
EMBL; AY165625; AAN87805.1; -
EMBL; AY046550; AAL05072.1; -
HSSP; Q92956; LJMA.
MGD; MGI:1930269; Tnftrsf23.
GO; GO:0005515; P:protein binding; IPI.
GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
DR InterPro; IPR001368; TNFR_C6; 3.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Glycoprotein; GPI-anchor; Lipoprotein; Receptor; Repeat; Signal.
FT SIGNAL 1 29
FT CHAIN 30 155
FT PROPEP 156 176 Tumor necrosis factor receptor
FT LIPID 155 155 superfamily member 23.
FT REPEAT 37 72 Removed in mature form (Potential).
FT REPEAT 74 114 GPI-anchor amidated cysteine (Potential).
FT REPEAT 115 155 TNFR-Cys 1.
FT REPEAT 115 155 TNFR-Cys 2.
FT DISULFID 38 49 TNFR-Cys 3.
FT DISULFID 50 63 By similarity.
FT DISULFID 53 72 By similarity.
FT DISULFID 75 90 By similarity.
FT DISULFID 93 106 By similarity.
FT DISULFID 96 114 By similarity.
FT DISULFID 116 131 By similarity.
FT DISULFID 134 147 By similarity.
FT DISULFID 137 155 By similarity.
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 176 AA; 19594 MW; EE30D617F49DDB7D CRC64;

Query Match 14.6%; Score 164.5; DB 1; Length 176;
Best Local Similarity 33.7%; Pred. No. 3.2e-06;
Matches 33; Conservative 15; Mismatches 41; Indels 9; Gaps 3;

Qy 47 CCRGCPAGHYLKAPCTPCGNGSTCLVCPQDFTFLAWENHNSECARQCACDEQASQVALEN 106
Db 49 CCKTGPSFTFVKAPCKIPHTQQCCKCHPGFTGKDNGLH-DCELCSCTCDKQNVVA--D 105

Qy 107 CSAVADTCGCKPGWFCVQSQVSSSPFFVCPQCLDC 144
Db 106 CSATSDRKCCEQIGLY-----YNDKPFESCRPCTKC 137

RESULT 5
Q8MJ20 ID Q8MJ20 PRELIMINARY; PRT; 130 AA.
AC Q8MJ20;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Fas receptor CD95 (Fragment).
OS Macaca mulatta (Rhesus macaque).

Query Match 14.6%; Score 164.5; DB 1; Length 176;
Best Local Similarity 33.7%; Pred. No. 3.2e-06;
Matches 33; Conservative 15; Mismatches 41; Indels 9; Gaps 3;

Qy 47 CCRGCPAGHYLKAPCTPCGNGSTCLVCPQDFTFLAWENHNSECARQCACDEQASQVALEN 106
Db 49 CCKTGPSFTFVKAPCKIPHTQQCCKCHPGFTGKDNGLH-DCELCSCTCDKQNVVA--D 105

Qy 107 CSAVADTCGCKPGWFCVQSQVSSSPFFVCPQCLDC 144
Db 106 CSATSDRKCCEQIGLY-----YNDKPFESCRPCTKC 137

RESULT 5
Q8MJ20 ID Q8MJ20 PRELIMINARY; PRT; 130 AA.
AC Q8MJ20;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Fas receptor CD95 (Fragment).
OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurrell B., Ameisen J.-C.,
RA Estaquier J.,
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530075; AAM95635.1; -
DR HSSP; O14763; 1DU3
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON TER 1 1
FT NON TER 130 130
FT NON TER 130 130
SQ SEQUENCE 130 AA; 14814 MW; 91542C61323F3C27 CRC64;

Query Match 14.3%; Score 161.5; DB 2; Length 130;
Best Local Similarity 31.7%; Pred. No. 4.5e-06;
Matches 32; Conservative 12; Mismatches 50; Indels 7; Gaps 1;

Qy 44 GLFCRCGCPAGHYLKAPCTPCGNGSTCLVCPQDFTFLAWENHNSECARQCACDEQASQVA 103
Db 22 GQFCRCGCPGGERKARDCTVNEDEPDVCPQEGKEYTDKGHFSKRCRLCDEGHGLEV 81

Qy 104 LENCASVADTCGCKPGWFCVQSQVSSSPFFVCPQCLDC 144
Db 82 EINCTRTQNTKCRCKPNFF-----CNSAVCEHCDCPCTKC 115

RESULT 6
Q911R5 ID Q911R5 PRELIMINARY; PRT; 186 AA.
AC Q911R5;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Tumour necrosis family receptor.
GN Name=A53R;
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=US87;
RX MEDLINE=21874859; PubMed=11878931; DOI=10.1006/viro.2001.1236;
RT "Vaccinia virus encodes a soluble and cell surface tumour necrosis
RT factor receptor that contributes to viral virulence."
RL Virology 292:285-298 (2002).
DR EMBL; AJ416893; CAC95181.2; -
DR HSSP; Q92956; LJMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR Pfam; PF00020; TNFR_C6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.

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DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR Reciprocal.
KW
SQ SEQUENCE 186 AA; 20662 MW; EF73D6A336A70C5A CRC64;

Query Match      13.9%; Score 157.5; DB 2; Length 186;
Best Local Similarity 28.4%; Pred. No. 1.3e-05;
Matches 4%; Conservative 17; Mismatches 64; Indels 25; Gaps 8;

QY 33 CDCAGDPHKIGLFCRCGPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARC 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 37 CD-EGEYLDKRNQCCNRCPPGEFAKVRCCGN-DNTKCRCPPHYTAIPNYSNG-CHQC 93

QY 93 QACDEQASQVALENCASVADTRCCKPGWFVECVQSCVSSSPYCPCLDGCGLHRHTR 152
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 94 RKCTPGSGFDKV--KCTGTQNSCKCLPGWYCATDSSQ-----TEDCRDC----- 135

QY 153 LLCSRRDTCGTCLPGFYEHGDG-CVSC 179

DB 136 --IPKRRCPCG-YFGGIDEQGNPTCKSC 160

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RESULT 7
Q9WJB4
ID Q9WJB4 PRELIMINARY; PRT; 186 AA.
AC Q9WJB4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumour necrosis factor receptor precursor.
GN Name=A53R;
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
CX NCBI_TaxID=10245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lister;
RC MEDLINE=99226947; PubMed=10211965;
RX Alcamì A., Khanna A., Paul N., Smith J.L.;
RT "Vaccinia virus strains Lister, USSR and Evans express soluble and
RL cell-surface tumour necrosis factor receptors.";
RL J. Gen. Virol. 80:949-959(1999).

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DR HSF1_Q22356; LUGA.
DR GO:0016020; C:membrane; IEA.
DR GO:0004888; F:transmembrane receptor activity; IEA.
DR GO:0006915; P:apoptosis; IEA.
DR GO:0006955; P:immune response; IEA.
DR GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; Fas receptor.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 2.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
DR Receptor; Signal.
FT SIGNAL 1 22 Potential.
SQ SEQUENCE 186 AA; 20646 MW; D93CD9180276EE31 CRC64;

Query Match 13.9%; Score 157.5; DB 2; Length 186;
Best Local Similarity 28.4%; Pred. No. 1.3e-05;
Matches 42; Conservative 17; Mismatches 64; Indels 25; Gaps 8

Qy	33	CDACGDDPHKIGLCECCGCPAGHYLKAPCTBPCNGNSTCLVCPQDTFLAWENHNSECARC	92
Db	37	CD-EGEYLDKRNHCQCCPGEFAKVRNCNGN-DNTKRCRCPDHYTAIPNYSNG-CHQC	93
Qy	93	QACDEQASQVALENCASAVADTRCCCKPGWFVECVQSVCSPPFCQCLPCDGAHLHRRH	152
Db	94	RKCPGTGSGFDKV--KCTGTQNSKCSCLPGWYCATDSSQ-----TEDCRDC-----	135

Qy 153 LLCRRDTCGTCLPGFYEHGDG-CVSC 179
:
||
||
||
Db 136 --IPKRRCPG-YFGGIDEQGNPICKSC 160
:
||
||
||
||

RESULT 8

O72735 PRELIMINARY; PRT; 186 AA.

AC O72735; 01-AUG-1998 (T-EMBLrel. 07, Created)

DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE A56R protein.

DE Name=A56R;

GN Cowpox virus (CPV).

OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OC NCBI_TaxID=10243;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=GRI-90;

RC MEDLINE=97068532; PubMed=8963248;

RX Saifonov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,

RA Shchelkunov S.N., Sandakhchiev L.S.;

RT "Genes of a circle of hosts for the cowpox virus.";

RL Dokl. Akad. Nauk 349:829-833(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=GRI-90;

RC MEDLINE=98239462; PubMed=9568042; DOI=10.1006/viro.1998.9039;

RX Ryzankina O.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,

RA Ryzankina O.I., Gutorov V.V., Kotwal G.J.;

RT "Species-specific differences in genome organization of cowpox,

RT smallpox, and vaccinia viruses.";

RL Virology 243:432-460(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=GRI-90;

RC Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Miheev M.V.,

RA Ryzankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,

RA Sandakhchiev L.S.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; X94355; CAD90723.1; -.

DR HSSP; Q92956; IJMA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR001368; TNFR.c6.

DR Pfam; PF00020; TNFR.c5; 2.

DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS00652; TNFR NGFR 1; UNKNOWN_2.

DR PROSITE; PS50050; TNFR NGFR 2; 2.

SO SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;

	Query Match	13.7%;	Score 155;	DB 2;	Length 186;	
	Best Local Similarity	23.9%;	Pred. No. 2.le-05;			
	Matches	39;	Conservative	20;	Mismatches 62;	Indels 42; Gaps 7
Qy	33	CDCAGDPHKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHSECARC	92			
Db	37	CD-EGEYLDKRHNQCNCQPGFEAKVRCS-GSDNTKCERCFFPHYTATIPNYSNG-CHQC	93			
Qy	93	OACDEQASQVALENCASAVADTRCCKPQGFVECCVSCVSPPFYCOPCLDGCGLHRHTR	152			
Db	94	RKPTGSGFDKV--KCTGTGNSKSCSLPGW-----CATD-----	125			

RESULT 9	
Q9YP87	
ID Q9YP87	PRELIMINARY;
AC Q9YP87;	PRT; 186 AA.

[illegible]

```
RX MEDLINE=99330195; PubMed=10403401; DOI=10.1016/S0014-5793(99)00683-3;
RA Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
RT "Cytokine-inducible CD40 gene expression in vascular smooth muscle
cells is mediated by nuclear factor kappaB and signal transducer and
activator of transcription-1.";
RL FEBS Lett. 453:191-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
RA Gao D., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF241231; AAFA43717.2; -.
DR HSSP; Q92956; 1JMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
FT NON TER 169
FT NON TER 169
SQ SEQUENCE 169 AA; 1825 MW; F199D91EFA224A26 CRC64;

Query Match 12.2%; Score 137.5; DB 2; Length 169;
Best Local Similarity 29.1%; Pred. No. 0.00058;
Matches 51; Conservative 15; Mismatches 78; Indels 31; Gaps 9;

Qy 5 PRGCAVAAMALLVLGARAAGGTRPRCDGAFHKKIGLFCRCGCPAGHYLKAPCTEP 64
Db 5 PQLCALMGCLLTAVHLG-----OCVTCSDKQYLQGGCCDLCPGNRLVSHCT-A 53

Qy 65 CGNSTCLVCPQDTFLAWENHNSE--CARQACD-EQASQVALENCASAVADTRCGCKPGW 121
Db 54 LEKTCQPCDGSERSA---HWNRIHQHCHCELNQLQVKKEG-TAVSDTVCTCKEG- 108

Qy 122 FVEQVQCQVSSSPFYCQPCLD----CGALHHRHRLCSRRDTCGTCCLPGFYEHG 173
Db 109 -----QHCASKE---CETCAQHRPCGPGFGVQWQMATETTTDVCQPCPVGFFSNG 154

RESULT 12
Q8SQ51 ID Q8SQ51 PRELIMINARY; PRT; 124 AA.
AC Q8SQ51
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fas deltae (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells.";
RL Eur. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072010; BAB86799.1; -.
DR HSSP; O14763; 1DQG.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6; 2.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;

Query Match 11.8%; Score 133.5; DB 2; Length 147;
Best Local Similarity 29.4%; Pred. No. 0.0011;
Matches 30; Conservative 12; Mismatches 23; Indels 37; Gaps 5;

Qy 83 NHNSCARQACDEQASQVALENCASAVADTRCGCKPGWFCVQVSCVSSSPFYCQPC 142
Db 10 SHFSPRCRCIKCDEEHGLEVEKNCTRTQNTKCKCKSNFP--CNVSQC-----DHCNPCM 62

Qy 143 DCGALHHRHRLCSRRDTCGTCCLPGFYEHG--DGCVCSCPTS 182
Db 63 MC-----EHGILENCT--PTS 76

RESULT 13
Q8SQ52 ID Q8SQ52 PRELIMINARY; PRT; 147 AA.
AC Q8SQ52
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fas (Fragment).
OC Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells.";
RL Eur. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072009; BAB86798.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;

Query Match 11.8%; Score 133.5; DB 2; Length 147;
Best Local Similarity 29.4%; Pred. No. 0.0011;
Matches 30; Conservative 12; Mismatches 23; Indels 37; Gaps 5;

Qy 83 NHNSCARQACDEQASQVALENCASAVADTRCGCKPGWFCVQVSCVSSSPFYCQPC 142
Db 10 SHFSPRCRCIKCDEEHGLEVEKNCTRTQNTKCKCKSNFP--CNVSQC-----DHCNPCM 62

Qy 143 DCGALHHRHRLCSRRDTCGTCCLPGFYEHG--DGCVCSCPTS 182
Db 63 MC-----EHGILENCT--PTS 76
```

```

DR ENBL; AF084992; AAF09112.1; -.
DR HSP; Q92956; IJMA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 176 AA; 19535 MW; 83C2168F1FD0B072 CRC64;

Query Match          11.3%; Score 128; DB 2; Length 176;
Best Local Similarity 33.3%; Pred.No. 0.0037;
Matches 31; Conservative 15; Mismatches 35; Indels 12; Gaps 6;

QY      26  GGTRSPRCAGDFHKKIGLFCRCGPCAGHYLKAPCTPCGCNSTDCLVCPDPTFLAWENHH 85
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db       18  GGSKM-----CKPD-EVKLGNCQCCPGCSGQKVTKVCTENS-ITCLCPNGTYLT--GLY 69

QY      86  NSECARCQACDEQASQVALENCASAVADTRCGCK 118
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db       70  N--CTNCTQCDD--TQTIVRNCTSTNTTICASK 98

Search completed: June 27, 2005, 13:59:20
Job time : 172 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2005, 13:44:28 ; Search time 162 Seconds
(without alignments)

465.545 Million cell updates/sec

Title: US-10-081-280-6_COPY_1_195

Perfect score: 1130

Sequence: 1 MEQPRGCAVAALLLVLL.....CVSPTTLGSPCPCRAA VC 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1426428

Minimum DB seq length: 0

Maximum DB seq length: 195

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1051	93.0	181	2	AAW26708 Human apo
2	1051	93.0	181	6	ABG73992 Human APO
3	1051	93.0	181	6	ABU08251 Human Apo
4	1051	93.0	181	6	ABG73857 Human Apo
5	1051	93.0	181	6	ABU10202 Human Apo
6	1051	93.0	181	6	ADA49687 Human Apo
7	1051	93.0	188	5	AAO17880 Human rhe
8	206.5	18.3	161	6	ABR62365 Tumour ne
9	200.5	17.7	154	3	AAAY94711 Tumour ne
10	200.5	17.7	154	6	ADA49698 Extracell
11	200.5	17.7	154	7	ADL17741 Human tum
12	200.5	17.7	154	8	ADJ56814 Human TNF
13	200.5	17.7	161	2	ABG74752 Human TNF
14	200.5	17.7	161	2	AAAR27496 Native 30
15	200.5	17.7	161	2	AAW59664 Human sol
16	200.5	17.7	161	2	AAW52267 Soluble t
17	200.5	17.7	161	2	AAW89233 Tumour ne
18	200.5	17.7	161	4	ABJ37676 Human 30
19	200.5	17.7	161	6	ABR62363 Tumour ne
20	200.5	17.7	161	6	ADA20577 Human 30k
21	200.5	17.7	161	6	ADA20579 Human 30k
22	200.5	17.7	161	8	ADH78698 Human tum
23	198.5	17.6	162	5	AAW48058 Human TNF
24	197.5	17.5	161	6	ABR62364 Tumour ne
25	197	17.4	32	4	AAW84943 Human TR3

26	196	17.3	139	4	AAB66977	Aab66977 Peptide:
27	196	17.3	139	5	ABG71825	Abg71825 Wild type
28	196	17.3	139	8	ADM28814	Adm28814 Human TNF
29	191	16.9	181	5	ABB98170	Abb98170 Soluble b
30	191	16.9	181	5	AAE25817	Aae25817 Bovine tu
31	190	16.8	32	8	ADH50950	Adh50950 Altered T
32	186	16.5	185	7	ADJ65993	Adj65993 Herpes vi
33	186	16.5	186	3	AAAY79206	AAy79206 Soluble h
34	186	16.5	186	6	ABU60688	Abu60688 Human sol
35	186	16.5	186	7	ADF50687	Adf50687 Soluble f
36	186	16.5	193	3	AAAY79204	Aay79204 Soluble h
37	186	16.5	193	6	ABU60675	Abu60675 Human sol
38	186	16.5	193	7	ADF50685	Adf50685 Soluble f
39	182	16.1	148	6	ABU60689	Abu60689 Human mat
40	182	16.1	155	6	ABU60676	Abu60676 Human mat
41	182	16.1	159	6	ABU60683	Abu60683 Human mat
42	175.5	15.5	159	2	AAAR24083	Aar24083 Truncated
43	175	15.5	170	3	ABJ36228	Abj36228 Rat Fas r
44	174.5	15.4	161	7	ADL17744	Adl17744 Human TRA
45	174.5	15.4	161	8	ADJ56817	Adj56817 Human TR2

ALIGNMENTS

RESULT 1
AAW26708
ID AAW26708 standard; protein; 181 AA.
XX
AC AAW26708;
XX
DT 14-APR-1998 (first entry)
XX
DE Human apoptosis protein Apo-2LI.
XX
KW Apo-2LI; apoptosis; Apo-2 ligand inhibitor; human; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Modified-site 67 /label= Sig_peptide
FT Modified-site 106 /note= "N-glycosylated"
FT Modified-site 106 /note= "N-glycosylated"
XX
PN WO9737020-A1.
XX
PD 09-OCT-1997.
XX
PF 31-MAR-1997; 97WO-US005230.
XX
PR 01-APR-1996; 96US-00625328.
PR 23-SEP-1996; 96US-00710802.
XX
(GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 1997-503105/46.
XX
N-ESDB; AAT91179.
XX
PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis in mammalian cells.
XX
PS Claim 1; Page 43-44; 70pp; English.
XX
CC This novel polypeptide, designated Apo-2 ligand inhibitor (Apo-2LI), can be used to inhibit apoptosis for therapeutic purposes. Its amino acid sequence was deduced from a human thymus cDNA clone (see AAT91179) and is identical to amino acid residues 1-181 of another novel apoptosis polypeptide, Apo-3 (see AAW26709). It may be a soluble, truncated of

CC secreted form of Apo-3, lacking some extracellular sequence as well as
CC the transmembrane and cytoplasmic sequences of Apo-3. Apo-2LI can be
CC produced in host cells using a claimed method. Chimeric polypeptides
CC comprising Apo-2LI fused to a heterologous amino acid sequence, and an
CC Apo-2LI dimer are also claimed. Apo-2LI can be used to inhibit mammalian
CC cell apoptosis in vivo or ex vivo, and in quantitative diagnostic assays
XX
SQ Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.8e-72;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180
DB 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180
QY 181 T 181
DB 181 T 181

RESULT 2
ABG73992
ID ABG73992 standard; protein; 181 AA.

AC ABG73992;
XX
XX 01-APR-2003 (first entry)
XX Human APO-2 ligand inhibitor (Apo2LI) protein.
XX
XX APO-2LI; human; apoptosis; monoclonal antibody; Apo-2 ligand inhibitor;
XX cytostatic; cancer; autoimmune; inflammatory; neurodegenerative disease.
XX
XX Homo sapiens.

XX US6469144-B1.
XX
XX 22-OCT-2002.
XX
XX 31-MAR-1997; 97US-00828683.
XX
XX 01-APR-1996; 96US-00625328.
XX 23-SEP-1996; 96US-00710802.
XX
XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;
XX
XX WPI; 2003-147110/14.
XX N-PSDB; ABX15839.
XX
XX Novel isolated monoclonal antibody useful for activating or stimulating
XX apoptosis in cancer cells, comprises an antigen binding site which binds
XX to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.
XX
XX Claim 1; Fig 1; 48pp; English.

XX This invention relates to an isolated monoclonal antibody comprising an
XX antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI)
XX polypeptide. The antibody of the invention may have cytostatic activity
XX and may act as an activator or stimulator of apoptosis in cancer cells,
XX as a blocker of excessive apoptosis or of the autoimmune/inflammatory
XX effects of Apo-3 resulting from nuclear factor (NF)-kappaB activation or

CC C-Jun-amino-terminal kinase (JNK) activation. The anti-Apo-2 ligand
CC inhibitor is useful in therapeutic purposes for activating or stimulating
CC apoptosis in cancer cells and may be used to block excessive apoptosis
CC (for example in neurodegenerative disease), or to block potential
CC autoimmune/inflammatory effects of Apo-3 resulting from nuclear factor
CC (NF)-kappaB activation or C-Jun-amino-terminal kinase (JNK) activation.
CC The antibody may also be used in diagnostic assays for Apo-2LI or Apo-3,
CC e.g. detecting Apo-2LI or Apo-3 expression in specific cells, tissues or
CC serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant
CC cell culture or natural sources. The present sequence represents the
CC human Apo-2 ligand inhibitor protein (Apo2-LI) which was used to generate
CC the antibody of the invention
XX

SQ Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.8e-72;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180
DB 121 WFVECVSQVSSSPFFYCQPCDCLGALHRRHRLILCSRRDTCGTLPGFYEHGDCVSCP 180
QY 181 T 181
DB 181 T 181

RESULT 3
ABU08251
ID ABU08251 standard; protein; 181 AA.

XX ABU08251;
XX
XX 13-MAY-2003 (first entry)
XX
XX Human Apo-2 ligand inhibitor, Apo-2LI.

XX Human; Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; AIDS;
XX acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer;
XX Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis;
XX retinitis pigmentosa; aplastic anaemia; cerebellar degeneration;
XX myocardial infarction; reperfusion injury; toxin-induced liver disease;
XX chromosome 1q36.3; programmed cell death.

XX Homo sapiens.
XX
XX US2002165157-A1.
XX
XX 07-NOV-2002.
XX
XX 21-FEB-2002; 2002US-00081280.
XX
XX 01-APR-1996; 96US-0014699P.
XX 23-SEP-1996; 96US-0026943P.
XX 31-MAR-1997; 97US-00829270.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;
XX
XX WPI; 2003-298703/29.
XX N-PSDB; ABX13176.
XX
XX New biologically active Apo-2LI or Apo-3 polypeptide, useful for

PT preparing a composition for treating cancer.

XX Claim 4; Fig 1; 45pp; English.

XX The invention relates to an new isolated biologically active Apo-2LI or
XX Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or
XX Apo-3 appearing as AB008251 and AB008252. Also included are a
XX chimeric molecule comprising the Apo-2LI fused to a heterologous amino
XX acid sequence; a dimer molecule comprising a first Apo-2LI and a second
XX Apo-2LI; an antibody that binds to Apo-2LI or Apo-3 (or to its
XX extracellular domain sequence), an isolated nucleic acid encoding Apo-2LI
XX or Apo-3, a vector comprising the nucleic acid, a host cell comprising
XX the vector, a method of producing Apo-2LI and a non-human (transgenic or
XX knockout) animal that contains cells that express nucleic acid encoding
XX Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3
XX are involved in apoptosis (programmed cell death) which is implicated in
XX AIDS, (acquired immunodeficiency syndrome), stroke, Alzheimer's disease,
XX Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis,
XX retinitis pigmentosa, aplastic anaemia, cerebellar degeneration,
XX myocardial infarction, reperfusion injury and toxin-induced liver
XX disease. The gene for both proteins is located on chromosome 1q36.3 Apo-
XX 2LI and Apo-3 are also useful for preparing a composition for treating
XX cancer. The present sequence represents Apo-2LI

XX Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.8e-72;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db |||||
Qy 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db |||||
Qy 61 CTEPCGNSTCLVCPQDTFLAENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db |||||
Qy 61 CTEPCGNSTCLVCPQDTFLAENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db |||||
Qy 121 WFVEQVQSQCSSSPFFYQCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
Db |||||
Qy 121 WFVEQVQSQCSSSPFFYQCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
Db |||||
Qy 181 T 181
Db 181 T 181

RESULT 4

ABG73857

ID ABG73857 standard; protein; 181 AA.

XX AC ABG73857;

XX DT 03-APR-2003 (first entry)

XX DE Human Apo-2 ligand inhibitor protein.

XX Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
XX tumour necrosis factor receptor; nuclear factor-kappa B; NF-kappa B;
XX Apo-2 ligand inhibitor; AIDS; acquired immunodeficiency syndrome;
XX Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;
XX aplastic anaemia; myocardial infarction; stroke; reperfusion injury;
XX toxin-induced liver disease; cancer; lupus; herpes virus infection.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 67

XX Modified-site /note= "N-glycosylated"

XX Modified-site 105

XX Modified-site /note= "N-glycosylated. The amino acid at residue 105 is
XX Glu not Asn"

XX US6462176-B1.

XX PD 08-OCT-2002.

XX PF 11-SEP-1997; 97US-00928069.

XX PR 23-SEP-1996; 96US-0026943P.

XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ;

XX DR WPI; 2003-173840/17.

XX DR N-PSDB; ABX15460.

XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
XX mammalian cells, for generating antibodies, in affinity purification
XX techniques, and in competitive-type receptor binding assays.

XX Example 1; Fig 1; 52pp; English.

XX The invention relates to an Apo-3 polypeptide having an extracellular
XX domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
XX has been found to stimulate or induce apoptotic activity in mammalian
XX cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
XX receptor (TNFR) family of polypeptides. The invention also relates to a
XX chimeric molecule comprising an extracellular domain sequence comprising
XX residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
XX Apo-3 polypeptide is useful therapeutically to induce apoptosis in
XX mammalian cells. Decreased levels of apoptosis has been associated with
XX conditions such as cancer, lupus, and herpes virus infection. Increased
XX levels of apoptosis are associated with diseases such as acquired
XX immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
XX disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
XX pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
XX infarction, stroke, reperfusion injury, and toxin-induced liver disease.
XX The Apo-3 polypeptide is also useful in non-therapeutic applications such
XX as in quantitative diagnostic assays as a control against which samples
XX containing unknown quantities of Apo-3 may be prepared, in generating
XX antibodies, as standards in assays for Apo-3, in affinity purification
XX techniques, and in competitive-type receptor binding assays. The chimeric
XX molecule is useful therapeutically to inhibit apoptosis or nuclear factor
XX -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
XX Apo-3 antibodies. The present sequence represents the human Apo-2 ligand
XX inhibitor protein which comprises amino acid residues 1 to 181 of the
XX human Apo-3 protein. It is believed that Apo-2 ligand inhibitor may be a
XX soluble, truncated or secreted form of Apo-3

XX Sequence 181 AA;

Query Match 93.0%; Score 1051; DB 6; Length 181;

Best Local Similarity 100.0%; Pred. No. 4.8e-72;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAENHNHNSCARCQACDEQASQVALENCSSAVADTRCGCKPG 120

Qy 121 WFVEQVQSQCSSSPFFYQCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Db 121 WFVEQVQSQCSSSPFFYQCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180

Qy 181 T 181

Db 181 T 181

RESULT 5

ABU10202
ID ABU10202 standard; protein; 181 AA.
XX
AC ABU10202;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human Apo-2 ligand inhibitor.
XX
KW Human; Apo-2 ligand inhibitor; apoptosis; gene therapy; inflammation;
KW cancer; neurodegenerative disease; immunosuppressive; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003004313-A1.
XX
PD 02-JAN-2003.
XX
PF 28-MAR-2002; 2002US-00112193.
XX
PR 23-SEP-1996; 96US-0026943P.
PR 11-SEP-1997; 97US-00928069.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 2003-438872/41.
DR N-PSDB; ACA61684.
XX
PT New isolated Apo-3 polypeptides, useful for stimulating or inducing
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
PT or ex vivo gene therapy techniques.
XX
PS Example 1; Fig 1; 50pp; English.
XX
CC The invention relates to an isolated Apo-3 polypeptide. The Apo-3
CC polypeptides are useful for stimulating or inducing apoptotic activity in
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
CC apoptosis, or as immunogens used in generating antibodies. The
CC antagonistic antibodies may be used to block excessive apoptosis, for
CC instance in neurodegenerative disease, or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from NP-kappaB activation. The
CC nucleic acid sequences are useful as diagnostics for tissue-specific
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
CC knockout animals.. The transgenic or knockout animals are useful in
CC developing and screening of therapeutically useful reagents. The present
CC sequence represents the amino acid sequence of human Apo-2 ligand
CC inhibitor
XX
SQ Sequence 181 AA;
Query Match 93.0%; Score 1051; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.8e-72;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVQCVSSSPFYCQPCLDGALHRRHRLTLCSRRDTCGTCLPGFYEHGCGVSCVP 180
Db 121 WFVECVQSVQCVSSSPFYCQPCLDGALHRRHRLTLCSRRDTCGTCLPGFYEHGCGVSCVP 180
Qy 181 T 181
Db 181 T 181

RESULT 6
ADA49687
ID ADA49687 standard; protein; 181 AA.
XX
AC ADA49687;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human Apo-2 ligand inhibitor (Apo-2LI) .
XX
KW Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;
KW competitive-type receptor; binding assay; cancer cell; human; cytostatic.
XX
OS Homo sapiens.
XX
PN US2002192729-A1.
XX
PD 19-DEC-2002.
XX
PF 28-MAR-2002; 2002US-00112793.
XX
PR 01-APR-1996; 96US-00625328.
PR 23-SEP-1996; 96US-00710802.
PR 31-MAR-1997; 97US-00828683.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 2003-657226/62.
DR N-PSDB; ADA49691.
XX
PT Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
PT in diagnostic assays.
XX
PS Claim 4; Fig 1; 53pp; English.
XX
CC The present invention relates to the isolation of a biologically active
CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide
CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The
CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI
CC is useful for generating antibodies, as standards in assays for Apo-3 or
CC Apo-2LI, in affinity purification techniques, and in competitive-type
CC receptor binding assays when labelled with radioiodine, enzymes or
CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
CC inducing apoptosis in cancer cells, and thus have therapeutic utility.
CC The present sequence represents human Apo-2LI.
XX
SQ Sequence 181 AA;
Query Match 93.0%; Score 1051; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.8e-72;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVQCVSSSPFYCQPCLDGALHRRHRLTLCSRRDTCGTCLPGFYEHGCGVSCVP 180
Db 121 WFVECVQSVQCVSSSPFYCQPCLDGALHRRHRLTLCSRRDTCGTCLPGFYEHGCGVSCVP 180
Qy 181 T 181
Db 181 T 181

```
RESULT 7
AAO17880
ID AAO17880 standard; protein; 188 AA.
XX
AC AAO17880;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related protein #2.
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200234912-A1.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-JP009313.
XX
PR 24-OCT-2000; 2000JP-00324296.
XX
PR 27-MAR-2001; 2001JP-00090546.
XX
PR 30-MAR-2001; 2001JP-00099990.
XX
PA (NEWI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
XX WPI; 2002-417132/44.
DR N-PSDB; AAL47187.
XX
XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies.
XX
XX Disclosure; Page 72-73; 84pp; Japanese.
PS
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a protein described in the exemplification of the invention
XX
XX Sequence 188 AA;
Query Match 93.0%; Score 1051; DB 5; Length 188;
Best Local Similarity 100.0%; Pred. No. 5e-72;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAAALLLVLLGARAOGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Dd 1 MEQPRGCAVAAALLLVLLGARAOGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG 120
Dd 61 CTEPCGNTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQCVSSSPFYCQPCDCLDGCALHRTLLCSRRDTCGTCLPGFYHGDGCVSCP 180
Dd 121 WFVEQVQCVSSSPFYCQPCDCLDGCALHRTLLCSRRDTCGTCLPGFYHGDGCVSCP 180
QY 181 T 181
Dd 181 T 181
RESULT 8
ABR62365
ID ABR62365 standard; protein; 161 AA.
XX
AC ABR62365;
XX
```

```
XX
DT 22-SEP-2003 (first entry)
XX
DE Tumour necrosis factor receptor extracellular domain H23P mutant.
XX
KW Tumour necrosis factor; receptor; TNFRF; proline; protein engineering;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 23 /note= "wild-type His substituted by Pro"
FT Misc-difference 46 /note= "wild-type Ser substituted by Ile"
XX
PN WO2003046160-A2.
XX
XX 05-JUN-2003.
XX
PF 21-NOV-2002; 2002WO-EP013059.
XX
PR 30-NOV-2001; 2001US-0340648P.
XX
XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Brondyk W, Jiang X, Schweickhardt RL;
XX
XX WPI; 2003-523245/49.
XX
XX Increasing expression of a protein, comprises substituting at least one
XX codon in the polynucleotide encoding the protein, for a codon encoding
XX proline.
PS
XX Example 2; Page; 53pp; English.
XX
XX This is the protein sequence of a mutated extracellular domain of the p55
XX tumour necrosis factor receptor (TNFRF) in which a Pro residue
XX substitutes the native His-34 residue (residue 23 in the present
XX sequence) and an Ile residue substitutes the native Ser-57 residue
XX (residue 46 of the present sequence). Screening of TNFRF mutant clones
XX using a yeast display system yielded a clone that showed a higher
XX expression level in yeast than did a wild-type TNFRF clone. The encoded
XX polypeptide contained these 2 amino acid substitutions. The introduction
XX of proline residues may assist the polypeptide to adopt a favourable
XX conformation that fixes the neighbouring cysteine residue into the
XX correct orientation for disulfide bond formation, resulting in a higher
XX yield of correctly folded proteins in yeast or mammalian host cells. The
XX invention therefore provides methods of increasing protein expression
XX levels by substituting an amino acid residue with proline, where the
XX substitution occurs within 15 (preferably within 10, and especially
XX within 5) amino acids of a cysteine residue. Note: The present sequence
XX is not shown in the specification but is derived from the TNFRF sequence
XX given in figure 4 (see ABR62363)
XX
XX Sequence 161 AA;
Query Match 18.3%; Score 206.5; DB 6; Length 161;
Best Local Similarity 30.4%; Pred. No. 4.4e-08;
Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;
QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWENHNHNSCARQACDQQA 99
Dd 11 HPQNNSTCCTKCPKGYLYNDPCPGPGQDTCREIGSFTASENHLR-HCLSCSKCKREM 69
QY 100 SQVALENCNSAVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCDCLDGCALHRTLLCS 156
Dd 70 GQVEISSCTVDRTVCGCRKQRYHNSENLFCQ-----FNCSLCLN-GTVH----LSCQ 119
QY 157 RRDTCGTCCLPGFYHGDGCVSCPSTLGSQCP---RCAAVC 195
Dd 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155
```

RESULT 9
AAY94711
ID AAY94711 standard; protein; 154 AA.
XX AC AAY94711;
XX DT 29-JAN-2001 (first entry)
XX XX Tumour necrosis factor receptor (TNFR) domain of TNFR-1.
DE
XX Tumour necrosis factor-receptor related protein; TR2; human; cancer;
KW chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
KW severely combined immunodeficiency; apoptosis inhibition;
KW Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
OS Homo sapiens.
XX WO200056405-A2.
PN
XX
XX 28-SEP-2000.
PD
XX
XX 22-MAR-2000; 2000WO-US007521.
XX
XX 22-MAR-1999; 99US-0125683P.
XX 26-MAR-1999; 99US-0126522P.
XX 20-MAY-1999; 99US-0135169P.
XX 06-AUG-1999; 99US-0147383P.
XX
XX (NIJ/J) NI J.
XX (ROSE/) ROSEN C A.
XX (GENTZ/) GENTZ R L.
XX
XX Ni J, Rosen CA, Gentz RL;
XX WPI; 2000-594519/56.
XX
XX Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
XX and its two splice variants, useful for treating arthritis or
XX inflammation, cancer (such as follicular lymphomas) and immunodeficiency
XX disorders.
XX
XX Disclosure; Fig 16; 373pp; English.
XX
XX This invention relates to an isolated nucleic acid molecule encoding a
XX human tumor necrosis factor (TNF)-receptor related protein TR2. Included
XX in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
XX The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
XX member of the TNFR superfamily. The invention includes a method for the
XX treatment of arthritis or inflammation using an antibody directed against
XX a fragment of the TR2 protein. TR2 is agonists, antagonists and
XX antibodies exhibit cytostatic, dermatological, antianaemic,
XX immunosuppressive, anti-allergic, antiarthritic, antidiabetic,
XX anti-inflammatory, neuroprotective, nootropic, antiparkinsonian, and
XX cerebroprotective activity. The methods are useful for treating arthritis
XX or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
XX mutations, cardiac tumours, pancreatic, breast, or prostate cancer), an
XX immunodeficiency or for enhancing an in vivo leukocyte response to an
XX antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
XX preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
XX dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
XX inflammatory myopathies) and immunodeficiency disorders (such as severely
XX combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
XX disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
XX TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
XX antagonists are useful for treating or preventing autoimmune diseases and
XX inhibit the growth, progression and/or metastasis of cancers. They are
XX also used to activate, differentiate or proliferate cancerous cells or
XX tissues, and can be used to treat diseases associated with increased cell
XX survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
XX Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful

CC as sources for generating antibodies, as molecular weight markers. This
CC sequence represents the tumour necrosis factor receptor (TNFR) domain of
CC the human TNFR-1 protein. The sequence was used in the characterisation
CC of the TR2 receptor protein of the invention
XX
SQ Sequence 154 AA;
Query Match 17.7%; Score 200.5; DB 3; Length 154;
Best Local Similarity 29.8%; Pred No. 1.2e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWNHNNHNSCARQACDEQA 99
Db 9 HPQNNSSICCTKCHKGTLYLNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCRKEM 67
QY 100 SQVALENCNSAVATRCGCKPGWFEVC---QVSQCVSSSPFYCQCLDGCALHRRHRLCLS 156
Db 68 GQVEISSCTVDRDTCGCRKNQRYHWSENLFCQ-----FNCSLCLN-GTVH-----LSCQ 117
QY 157 RRDTCGTCLPGFVEHGDGCVSPTSTLGSCE--RCAAVC 195
Db 118 EKQNTVCTCHAGFLRENECVSC-----SNCKSLECTKLC 153
RESULT 10
ADA49698
ID ADA49698 standard; protein; 154 AA.
XX AC ADA49698;
XX DT 20-NOV-2003 (first entry)
XX DE Extracellular region of human TNFR1 (htnfr1) protein.
XX KW Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;
XX competitive-type receptor; binding assay; cancer cell; human;
XX TNF receptor family; htnfr1; cytostatic.
XX OS Homo sapiens.
XX FN US2002192729-A1.
XX PD 19-DEC-2002.
XX PF 28-MAR-2002; 2002US-00112793.
XX PR 01-APR-1996; 96US-00625328.
XX PR 23-SEP-1996; 96US-00710802.
XX PR 31-MAR-1997; 97US-00828683.
XX PA (GETH) GENENTECH INC.
XX FI Ashkenazi AJ;
XX WPI; 2003-657226/62.
XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
XX Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
XX in diagnostic assays.
XX Disclosure; Fig 2; 53pp; English.
XX The present invention relates to the isolation of a biologically active
XX Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide
XX sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The
XX Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI
XX is useful for generating antibodies, as standards in assays for Apo-3 or
XX Apo-2LI, in affinity purification techniques, and in competitive-type
XX receptor binding assays when labelled with radioiodine, enzymes or
XX fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
XX inducing apoptosis in cancer cells, and thus have therapeutic utility.
XX The present sequence represents the extracellular region of a human TNF
XX receptor family protein. This sequence is compared with the extracellular

```
CC region of human Apo-2LI.
XX Sequence 154 AA;
SQ
  Query Match      17.7%; Score 200.5; DB 6; Length 154;
  Best Local Similarity 29.8%; Pred. No. 1.2e-07;
  Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 99
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESSGFTASENHLR-HCLSCSKCKREM 67
QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCLS 156
Db 68 GQVEISSCTVDRTVCGCRKNQYRHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
QY 157 RRDTCGTCGPGFYEHDGCVSCPTSTLGSCEP--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153

RESULT 11
ID ADL17741 standard; protein; 154 AA.
XX
AC ADL17741;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human tumour necrosis factor receptor-I cysteine rich motif.
XX
KW Human; apoptosis inducing molecule II; AIM II; antibody;
KW tumour necrosis ligand superfamily; lymphotoxin-beta receptor; TR6;
KW TRAIL receptor 6; lymphadenopathy; aberrant bone development;
KW autoimmune disease; graft-versus-host disease; rheumatoid arthritis;
KW osteoarthritis; cancer; apoptosis.
XX
OS Homo sapiens.
XX
PN US6635743-B1.
XX
PD 21-OCT-2003.
XX
PP 10-MAR-2000; 2000US-00523323.
XX
PR 22-MAR-1996; 96US-0013923P.
PR 31-OCT-1996; 96US-0030157P.
PR 21-MAR-1997; 97US-00822953.
PR 07-JAN-1998; 98US-00003886.
PR 20-FEB-1998; 98US-00027287.
PR 19-FEB-1999; 98US-0075409P.
PR 11-MAR-1999; 99US-0124041P.
PR 04-JUN-1999; 99US-0137457P.
PR 06-JUL-1999; 99US-0142657P.
PR 11-AUG-1999; 99US-0148326P.
PR 02-DEC-1999; 99US-0168380P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Yu G, Ruben SM, Ullrich S, Zhai Y;
XX
XX WPI; 2003-810570/76.
XX
PT New antibody that binds to human Apoptosis Inducing Molecule II (AIM II)
PT protein, useful for preparing a composition for treating e.g.,
PT lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis
PT or cancer.
XX
PS Example 13; SEQ ID NO 53; 163pp; English.
XX
CC The invention relates to an isolated antibody or its portion binding to a
CC protein comprising a protein whose sequence comprises an immunogenic
```

```
CC fragment of the amino acid residues 68-240 of the Human apoptosis
CC inducing molecule II, AIM II, appearing as ADL17690 or a protein whose
CC sequence comprises a fragment of amino acid residues 68-240, where the
CC fragment comprises at least 30 or 50 amino acid residues. Also included
CC are a hybridoma that produces the antibody, a method of detecting in a
CC biological sample a protein that binds the antibody or its portion, a
CC composition comprising the antibody and a carrier and an isolated cell
CC that produces the antibody. Human AIM II is a member of the tumour
CC necrosis ligand superfamily and has been shown to bind lymphotoxin-beta
CC receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing
CC a composition for treating e.g., lymphadenopathy, aberrant bone
CC development, autoimmune disease, graft-versus-host disease, rheumatoid
CC arthritis, osteoarthritis or cancer (many other diseases and conditions
CC are listed in the specification). The present sequence represents a
CC cysteine-rich motif from a protein thought to bind AIM II.
XX
SQ Sequence 154 AA;
  Query Match      17.7%; Score 200.5; DB 7; Length 154;
  Best Local Similarity 29.8%; Pred. No. 1.2e-07;
  Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 99
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESSGFTASENHLR-HCLSCSKCKREM 67
QY 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCLS 156
Db 68 GQVEISSCTVDRTVCGCRKNQYRHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
QY 157 RRDTCGTCGPGFYEHDGCVSCPTSTLGSCEP--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153

RESULT 12
ADJ56814
ID ADJ56814 standard; protein; 154 AA.
XX
AC ADJ56814;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human TNFR-I cysteine-rich motif.
XX
KW Apoptosis inducing molecule II; AIM II; TNF; tumour necrosis factor;
KW therapy; graft versus host disease; immunodeficiency; cancer;
KW autoimmune disease; multiple sclerosis; type I diabetes;
KW rheumatoid arthritis; primary biliary cirrhosis; aplastic anaemia;
KW myelodysplasia; systemic lupus erythematosus;
KW idiopathic thrombocytopenic purpura; cellular response;
KW T-cell activation; molecular weight marker; human; TNF receptor; TNFR.
XX
OS Homo sapiens.
XX
PN US2004009147-A1.
XX
PD 15-JAN-2004.
XX
PP 28-FEB-2003; 2003US-00375680.
XX
PR 22-MAR-1996; 96US-0013923P.
PR 31-OCT-1996; 96US-0030157P.
PR 21-MAR-1997; 97US-00822953.
PR 07-JAN-1998; 98US-00003886.
PR 20-FEB-1998; 98US-00027287.
PR 20-FEB-1998; 98US-0075409P.
PR 19-FEB-1999; 99US-00252656.
PR 11-MAR-1999; 99US-0124041P.
PR 04-JUN-1999; 99US-0137457P.
PR 06-JUL-1999; 99US-0142657P.
PR 11-AUG-1999; 99US-0148326P.
PR 02-DEC-1999; 99US-0168380P.
```


PS Claim 54; Fig 2; 100pp; English.

XX The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor moles. may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmacokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct CC PN field.)

XX SQ Sequence 161 AA;

Query Match 17.7%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.2e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 99
Db 11 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKKEM 69

Qy 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCLS 156
Db 70 GQVEISSCTVDRDTCGCRKNQYRHWYSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

Qy 157 RRDTCGTCCLFGFHYHGDGVCSCPTSTILGSCPE--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLLECTKLC 155

RESULT 15
AAW59664
ID AAW59664 standard; protein; 161 AA.
AC AAW59664;
XX
XX 28-SEP-1998 (first entry)
XX Human soluble tumour necrosis factor receptor type I.
XX Human; tumour necrosis factor; TNF; TNF receptor type I;
KW inflammatory disease; leukaemia; TNF binding protein;
KW anti-inflammatory drug; methotrexates.
XX Homo sapiens.
XX
XX WO9824463-A2.
XX
XX 11-JUN-1998.
XX
XX 08-DEC-1997; 97WO-US022733.
XX
XX 06-DEC-1996; 96US-0032587P.
XX 23-JAN-1997; 97US-0036355P.
XX 07-FEB-1997; 97US-0039315P.
XX 09-JUL-1997; 97US-0052023P.
XX (AMGE-) AMGEN INC.
XX
XX Bendele AM, Sennello RM, Edwards CK;
XX
XX WPI; 1998-333039/29.
XX N-PSDB; AAV41548.
XX
XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.

XX PS Disclosure; Fig 1; 104pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate

XX SQ Sequence 161 AA;

Query Match 17.7%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.2e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 99
Db 11 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKKEM 69

Qy 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCLS 156
Db 70 GQVEISSCTVDRDTCGCRKNQYRHWYSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

Qy 157 RRDTCGTCCLFGFHYHGDGVCSCPTSTILGSCPE--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLLECTKLC 155

Search completed: June 27, 2005, 14:02:08
Job time : 164 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:02:25 ; Search time 162 Seconds
(without alignments)
462.882 Million cell updates/sec

Title: US-10-081-280-6_COPY_1_195

Perfect score: 1130

Sequence: 1 MEQPRGCAVAAALLLVLL.....CVSCPTSTLGSRCRAVC 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1055982

Minimum DB seq length: 0

Maximum DB seq length: 195

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1051	93.0	181	9	US-09-884-733-1
2	1051	93.0	181	9	US-09-993-234-1
3	1051	93.0	181	13	US-10-081-280-1
4	1051	93.0	181	13	US-10-112-793-1
5	1051	93.0	181	14	US-10-112-793-1
6	1051	93.0	188	15	US-10-415-247-5
7	210.5	18.6	162	9	US-09-798-789-12
8	210.5	18.6	162	14	US-10-218-102-422
9	209.5	18.5	190	9	US-09-899-429A-18
10	205.5	18.2	162	9	US-09-798-789-13
11	205.5	18.2	162	9	US-09-798-789-20
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 5, Appli
					Sequence 12, Appl
					Sequence 422, App
					Sequence 18, Appl
					Sequence 13, Appl
					Sequence 20, Appl

12	205.5	18.2	162	14	US-10-218-102-423	Sequence 423, App
13	205.5	18.2	162	14	US-10-218-102-430	Sequence 430, App
14	205	18.1	173	9	US-09-899-429A-16	Sequence 16, Appl
15	205	18.1	183	9	US-09-899-429A-10	Sequence 10, Appl
16	203.5	18.0	162	9	US-09-798-789-11	Sequence 11, Appl
17	203.5	18.0	162	14	US-10-218-102-421	Sequence 421, App
18	201.5	17.8	162	9	US-09-798-789-19	Sequence 19, Appl
19	201.5	17.8	162	9	US-09-798-789-21	Sequence 21, Appl
20	201.5	17.8	162	14	US-10-218-102-429	Sequence 429, App
21	201.5	17.8	162	14	US-10-218-102-431	Sequence 431, App
22	200.5	17.7	153	9	US-09-800-909-3	Sequence 3, Appli
23	200.5	17.7	153	9	US-09-884-987-4	Sequence 4, Appli
24	200.5	17.7	153	9	US-09-800-908-12	Sequence 12, Appli
25	200.5	17.7	153	15	US-10-423-927-3	Sequence 3, Appli
26	200.5	17.7	153	16	US-10-632-929-12	Sequence 12, Appl
27	200.5	17.7	154	13	US-10-112-793-12	Sequence 12, Appl
28	200.5	17.7	154	15	US-10-375-680-53	Sequence 53, Appl
29	200.5	17.7	161	9	US-09-899-422-4	Sequence 4, Appli
30	200.5	17.7	161	9	US-09-907-263-2	Sequence 2, Appli
31	200.5	17.7	161	9	US-09-898-234-4	Sequence 4, Appli
32	200.5	17.7	161	9	US-09-899-429A-4	Sequence 4, Appli
33	200.5	17.7	161	9	US-09-792-356-4	Sequence 4, Appli
34	200.5	17.7	161	10	US-09-882-735-2	Sequence 2, Appli
35	200.5	17.7	161	14	US-10-436-826-73	Sequence 73, Appl
36	200.5	17.7	161	15	US-10-621-783-2	Sequence 2, Appli
37	200.5	17.7	161	15	US-10-622-383-2	Sequence 2, Appli
38	200.5	17.7	161	17	US-10-496-218-1	Sequence 1, Appli
39	200.5	17.7	162	9	US-09-798-789-9	Sequence 9, Appli
40	200.5	17.7	162	9	US-09-798-789-14	Sequence 14, Appl
41	200.5	17.7	162	9	US-09-798-789-22	Sequence 22, Appl
42	200.5	17.7	162	9	US-09-899-429A-6	Sequence 6, Appli
43	200.5	17.7	162	14	US-10-218-102-419	Sequence 419, App
44	200.5	17.7	162	14	US-10-218-102-424	Sequence 424, App
45	200.5	17.7	162	14	US-10-218-102-432	Sequence 432, App

ALIGNMENTS

RESULT 1

Sequence 1, Application US/09884733
Patent No. US20020123116A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 Ligand Inhibitor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,733
FILING DATE: 19-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/304,003
FILING DATE: 14-JUNE-2000
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-884-733-1

Query Match 93.0%; Score 1051; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCSSAVADTRCGCKPG 120
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DB 121 WFVECVSQCVSSSPFFYQPCDCLDGCALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180

QY 181 T 181
DB 181 T 181

RESULT 2
US-09-993-234-1
; Sequence 1, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-993-234-1

Query Match 93.0%; Score 1051; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVECVSQCVSSSPFFYQPCDCLDGCALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180
DB 121 WFVECVSQCVSSSPFFYQPCDCLDGCALHRRHRLTLLCSRRDTCGTCPLPGFYEHGDCVSCP 180

QY 181 T 181
DB 181 T 181

RESULT 3
US-10-081-280-1
; Sequence 1, Application US/10081280
; Publication No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-081-280-1

Query Match 93.0%; Score 1051; DB 13; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCSSAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
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RESULT 4

US-10-112-793-1
; Sequence 1, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-112-793-1

Query Match 93.0%; Score 1051; DB 13; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
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Db 121 WFVEQVQSQVSSSPFYCQPCDCLDGCALHRRHRLLCSSRRDTCGTCGLPGFYEHGDCVSCP 180

Qy 181 T 181
Db 181 T 181

RESULT 5

US-10-112-193-1
; Sequence 1, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,193
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-112-193-1

Query Match 93.0%; Score 1051; DB 14; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.8e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCSSAVADTRCGCKPG 120
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Db 121 WFVEQVQSQVSSSPFYCQPCDCLDGCALHRRHRLLCSSRRDTCGTCGLPGFYEHGDCVSCP 180
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Db 181 T 181

RESULT 6

US-10-415-247-5

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; Sequence 5, Application US/10415247
; Publication No. US20040013655A1
; GENERAL INFORMATION:
; APPLICANT: Shiozawa, Shunichi
; TITLE OF INVENTION: Genome responsible for chronic rheumatoid arthritis,
; TITLE OF INVENTION: diagnostic method, pathogenicity judging method and
; TITLE OF INVENTION: detection-use diagnostic kit of chronic rheumatoid
; TITLE OF INVENTION: arthritis, and therapeutic method and medicine of
; TITLE OF INVENTION: chronic rheumatoid arthritis
; FILE REFERENCE: TLOPI-2
; CURRENT APPLICATION NUMBER: US/10/415,247
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2000-324296
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: JP 2001-90546
; PRIOR FILING DATE: 2001-3-27
; PRIOR APPLICATION NUMBER: JP 2001-99990
; PRIOR FILING DATE: 2001-3-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-247-5

Query Match      93.0%; Score 1051; DB 15; Length 188;
Best Local Similarity 100.0%; Pred. No. 5.9e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
Db 1 MEQPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFTLAWENHNHNSCARCQACDSQASQVALENCSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFTLAWENHNHNSCARCQACDEQASQVALENCSAVADTRCGCKPG 120

Qy 121 WFEVCQSVQCVSSSPFYCOPCLDCGALHRHRLICSRDTCGTCPLGFGYEHGDCVSCP 180
Db 121 WFEVCQSVQCVSSSPFYCOPCLDCGALHRHRLICSRDTCGTCPLGFGYEHGDCVSCP 180

Qy 181 T 181
Db 181 T 181

RESULT 7
US-09-798-789-12
; Sequence 12, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFI/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-12

Query Match      18.6%; Score 210.5; DB 9; Length 162;
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Best Local Similarity 30.0%; Pred. No. 3.4e-09;
Matches 48; Conservative 20; Mismatches 73; Indels 19; Gaps 6;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTEPCGNSTCLVCPQDTFTLAWENHNHNSCARCQACDEQA 99
Db 12 HPQNNISICCTKCHKGTLYNDPCPGQDTCRECESGSFTASE-EHKRECLRCRCRDKM 70

Qy 100 SQVALENCSAVADTRCGCKPGWFEVCQSVQCVSSSPFYCOPCLDC--GALHRHRLICSR 157
Db 71 GQVEISSCTVDRDVTVCGRKN-----QYRHYETENEFFCFNCSLCNGTVH----LSCQE 121

Qy 158 RDTDCGTCPLGFGYEHGDCVSCPTSTLGSQPE--RCAAVC 195
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 8
US-10-218-102-422
; Sequence 422, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFI/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 422
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-422

Query Match      18.6%; Score 210.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 3.4e-09;
Matches 48; Conservative 20; Mismatches 73; Indels 19; Gaps 6;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTEPCGNSTCLVCPQDTFTLAWENHNHNSCARCQACDEQA 99
Db 12 HPQNNISICCTKCHKGTLYNDPCPGQDTCRECESGSFTASE-EHKRECLRCRCRDKM 70

Qy 100 SQVALENCSAVADTRCGCKPGWFEVCQSVQCVSSSPFYCOPCLDC--GALHRHRLICSR 157
Db 71 GQVEISSCTVDRDVTVCGRKN-----QYRHYETENEFFCFNCSLCNGTVH----LSCQE 121

Qy 158 RDTDCGTCPLGFGYEHGDCVSCPTSTLGSQPE--RCAAVC 195
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 9
US-09-899-429A-18
; Sequence 18, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
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RESULT 10
US-09-798-789-13
; Sequence 13, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahivat, Bassil
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence

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Query Match	18.2%	Score	205.5	DB	9	Length	162
Best Local Similarity	30.4%	Pred. No.	8.5e-09				
Matches	49	Conservative	20	Mismatches	71	Indels	21
						Gaps	7
Qy	40	HKKIGLFCRCRCPAGHYLKAPCTSPCGNSTCLVCPQDTFLAWENHHNSECRCQACDEQA	99				
Db	12	HPQNNISCCCTVCHGTYLYNDPCGGQDTCRECSGFTASENHLR-HCLSCSKCKREM	70				
Qy	100	SQVALENCASVADTRCGCKPGWFVECQ---VSQCVSSSPFYCQPCLDGCALHRHRTLCS	156				
Db	71	GOVEISSCTVDRDVCGRKNQYRHYQSENLFQC-----FNCSLCLN-GTVH-----LSCQ	120				
Qy	157	RRDTDGCTCLPGFVHGDCVCSPSTSLGSCP E--RCAAVC	195				
Db	121	EKONTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC	156				

RESULT 12
US-10-218-102-423
; Sequence 423, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost

; TITLE OF INVENTION: Protein Design Automation for Protein Libraries

; FILE REFERENCE: A-67229-11/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 423
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; US-10-218-102-423

Query Match 18.2%; Score 205.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 8.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 40 HKKIGLFCRCRCPAGHYLKAPCTEPCGNSSTCLVCPQDTFLAWENHNHSECARCOACDEQA 99
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-DCLQCSQCKKHD 70

Qy 100 SOVALENCASAVADTRCGCKPWFVEVCQ---VSQCVSSSPFYCQCLDCGALHRRHRLCSR 157
Db 71 GQVEISSCTVDRTVCGCRKN-----QYRHYDHNRYFCNCSLCLNGTVH-----LSCQE 121

Qy 158 RDTDCGTCPLPGFYEHGDCVSCPTSTLGSQPE--RCAAVC 195
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 13

US-10-218-102-430
; Sequence 430, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost

; TITLE OF INVENTION: Protein Design Automation for Protein Libraries

; FILE REFERENCE: A-67229-11/RPT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 430
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic

US-10-218-102-430

Query Match 18.2%; Score 205.5; DB 14; Length 162;
Best Local Similarity 30.4%; Pred. No. 8.5e-09;
Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCRCPAGHYLKAPCTEPCGNSSTCLVCPQDTFLAWENHNHSECARCOACDEQA 99
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLUSCKSKREM 70

Qy 100 SOVALENCASAVADTRCGCKPWFVEVCQ---VSQCVSSSPFYCQCLDCGALHRRHRLCLS 156
Db 71 GQVEISSCTVDRTVCGCRKNQYRHYQSENLFCQ-----FNCSLCLN-GTVH-----LSCQ 120

Qy 157 RDTDCGTCPLPGFYEHGDCVSCPTSTLGSQPE--RCAAVC 195
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 14

US-09-899-429A-16
; Sequence 16, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Strutowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
; US-09-899-429A-16

Query Match 18.1%; Score 205; DB 9; Length 173;
Best Local Similarity 29.0%; Pred. No. 9.9e-09;
Matches 54; Conservative 23; Mismatches 85; Indels 24; Gaps 8;

Qy 15 LLLVLLGARAGGTRSPRCADGDFHKKIGLFCRCRCPAGHYLKAPCTEPCGNSSTCLVCP 74
Db 1 MLVPHLGDRK---RDSVCPQGYIHPQNNISCTCKCHKGTLYNDPCPGQDTCRECE 57

Qy 75 QDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPWFVEVC---QVSQCV 131
Db 58 SGSFTASENHLR-HCLSCSKCKREMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQC- 115

Qy 132 SSSPFYCQCLDCGALHRRHRLCSRRTDGTGTCPLPGFYEHGDCVSCPTSTLGSQPE-- 189
Db 116 -----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC-----SNCKKS 161

Qy 190 RCAAVC 195


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Db      | :|
162 ECTKLC 167

RESULT 15
US-09-899-429A-10
; Sequence 10, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Poggy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 10
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-10

Query Match      18.1%; Score 205; DB 9; Length 183;
Best Local Similarity 29.0%; Pred.No.1e-08;
Matches 54; Conservative 23; Mismatches 85; Indels 24; Gaps 8;

Qy      15  LLLVLLGARAGQGRSPRCDAGDFHKKIGLFCCRGCPCAGHYLKAPCTPCGNGSTCLVCP 74
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Qy      75  QDTFLAWNHNHNSCARCOAQDEQASQVALENCSAVADTRCGCKPGWFVEC---QVSQCV 131
Db      58  SGSEFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRTVCGCRKNQYRHYWSENLFQC- 115
Qy      132  SSSPFYCPCLDCGALHRRHTLLCSRRDTCGTCLPGFYEHDGCVSCPTLGCSPB-- 189
Db      116  ----FNCSLCLN-GRVH----LSCQEQNTVCTCHAGFFLRENECVSC-----SNCKSL 161
Qy      190  RCAAVC 195
Db      162  ECTKLC 167
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Title: US-10-081-280-6_COPY_1_195
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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2	1051	93.0	181	4	US-08-828-683A-1
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4	200.5	17.7	153	3	US-08-477-347-12
5	200.5	17.7	153	3	US-08-476-862-3
6	200.5	17.7	153	3	US-08-468-560C-4
7	200.5	17.7	153	4	US-09-800-909-3
8	200.5	17.7	153	4	US-09-800-908-12
9	200.5	17.7	154	4	US-08-828-683A-12
10	200.5	17.7	154	4	US-09-523-323-53
11	200.5	17.7	161	3	US-09-326-394-2
12	198.5	17.6	154	2	US-08-232-087A-10
13	196	17.3	139	3	US-08-706-945D-129
14	191	16.9	181	4	US-09-513-007-4
15	186	16.5	193	3	US-09-146-950-2
16	185	16.4	123	4	US-09-855-266A-13
17	182	16.1	155	3	US-09-146-950-4
18	182	16.1	159	3	US-09-146-950-20
19	175.5	15.5	158	1	US-08-050-319B-54
20	175.5	15.5	158	2	US-08-465-982-54
21	174.5	15.4	161	4	US-09-523-323-56
22	171.5	15.2	180	4	US-09-612-033B-10
23	166	14.7	167	1	US-08-050-319B-2
24	166	14.7	167	1	US-08-050-319B-57
25	166	14.7	167	2	US-08-465-982-2
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27	164.5	14.6	148	3	US-09-411-722-2

28	164.5	14.6	148	4	US-09-855-266A-2	Sequence 2, Appli
29	164.5	14.6	176	3	US-09-411-722-1	Sequence 1, Appli
30	164.5	14.6	176	4	US-09-855-266A-1	Sequence 1, Appli
31	162.5	14.4	119	2	US-08-219-237B-3	Sequence 3, Appli
32	162.5	14.4	119	3	US-08-477-347-14	Sequence 14, Appli
33	162.5	14.4	119	3	US-08-476-862-5	Sequence 5, Appli
34	162.5	14.4	119	3	US-08-468-560C-3	Sequence 3, Appli
35	162.5	14.4	119	4	US-08-828-683A-15	Sequence 15, Appli
36	162.5	14.4	119	4	US-09-800-909-5	Sequence 5, Appli
37	162.5	14.4	119	4	US-09-800-908-14	Sequence 14, Appli
38	162.5	14.4	128	3	US-09-180-100-9	Sequence 9, Appli
39	162.5	14.4	143	3	US-09-180-100-10	Sequence 10, Appli
40	162.5	14.4	144	3	US-09-180-100-21	Sequence 21, Appli
41	162.5	14.4	157	3	US-09-180-100-15	Sequence 15, Appli
42	162.5	14.4	159	3	US-09-180-100-23	Sequence 23, Appli
43	162.5	14.4	167	4	US-08-828-683A-22	Sequence 22, Appli
44	158.5	14.0	124	1	US-08-050-319B-4	Sequence 4, Appli
45	158.5	14.0	124	2	US-08-465-982-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-928-069-1
; Sequence 1, Application US/08928069
; Patent No. 6462176
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026943
; FILING DATE: 09/23/1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-928-069-1

Query Match 93.0%; Score 1051; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEQPRGCAVAALLVLLGARAQGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALLVLLGARAQGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSEACRQCACDEASQVALENCASVADTRCGCKPG 120

Db 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVECVQSQVSSPPFYCQCLDCGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSQVSSPPFYCQCLDCGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
QY 181 T 181
Db 181 T 181
RESULT 2
US-08-828-683A-1
; Sequence 1, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-828-683A-1
Query Match 93.0%; Score 1051; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVECVQSQVSSPPFYCQCLDCGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSQVSSPPFYCQCLDCGALHRRHRLTLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
QY 181 T 181

Db 181 T 181
RESULT 3
US-08-219-237B-4
; Sequence 4, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-4
Query Match 17.7%; Score 200.5; DB 2; Length 153;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWENHNSECARQACDEQA 99
Db 9 HPQNNISCTTKCHKGTLYNDGPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67
QY 100 SQVALENCSSAVADTRCGCKPGWFVECV---QVSCVSSSPFYCQCLDCGALHRRHRLTLLCS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
QY 157 RRDTDCGTCCLPGYEHGDCGVCSTLTGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSELECTKLC 153
RESULT 4
US-08-477-347-12
; Sequence 12, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: MEIT, Igor
; TITLE OF INVENTION: TNF LIGANDS

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.347
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115.685
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-347-12

Query Match 17.7%; Score 200.5; DB 3; Length 153;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 99
Db 9 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67
Qy 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQPCDCLGALHRHRLLCSS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
Qy 157 RRDTCGCLPGFVEHGDGVCVSCPTSLGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153

RESULT 5
US-08-476-862-3
Sequence 3, Application US/08476862
Patent No. 6262239
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-862-3

Query Match 17.7%; Score 200.5; DB 3; Length 153;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 40 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDQQA 99
Db 9 HPQNNISICTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67
Qy 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQPCDCLGALHRHRLLCSS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
Qy 157 RRDTCGCLPGFVEHGDGVCVSCPTSLGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153

RESULT 6
US-08-468-560C-4
Sequence 4, Application US/08468560C
Patent No. 6270998
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA

; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,560C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR., GERLAD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 20-4393P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-560C-4

Query Match 17.7%; Score 200.5; DB 3; Length 153;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSGTCVCPQDTFLAWENHNHNSCARCOACDEQA 99
Db 9 HPQNSICCTCKCHKGYLYNDGPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67

Qy 100 SQVALENCASAVATRCGCKPGWFVEC---QVSCQVSSSPFYCQPLDGCALHRRHRLCS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117

Qy 157 RRDTDCGTCCLPGFYEHGDCGVCSTLTGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 153

RESULT 7
US-08-900-909-3
; Sequence 3, Application US/09800909
; Patent No. 655511
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,862
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-800-909-3

Query Match 17.7%; Score 200.5; DB 4; Length 153;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSGTCVCPQDTFLAWENHNHNSCARCOACDEQA 99
Db 9 HPQNSICCTCKCHKGYLYNDGPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67

Qy 100 SQVALENCASAVATRCGCKPGWFVEC---QVSCQVSSSPFYCQPLDGCALHRRHRLCS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117

Qy 157 RRDTDCGTCCLPGFYEHGDCGVCSTLTGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 153

RESULT 8
US-09-800-908-12
; Sequence 12, Application US/09800908
; Patent No. 6602993
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,908
; FILING DATE: 08-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,347

FILING DATE: <Unknown>
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-800-908-12
Query Match 17.7%; Score 200.5; DB 4; Length 153;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQA 99
Db 9 HPQNNISCTCKHGTLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 67
QY 100 SOVALENCASAVADTRCGCKPGWFVEC---QVSQCVSPPFYCQCLDGCALHRHRLCLS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCIN-GTVH----LSCQ 117
QY 157 RRDTDCGTCCLPGFVEHGDGVCSTPTSLGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENEVCSC-----SNCKKSLECTKLC 153
RESULT 9
US-08-828-683A-12
Sequence 12, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-828-683A-12
Query Match 17.7%; Score 200.5; DB 4; Length 154;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARCQACDQA 99
Db 9 HPQNNISCTCKHGTLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 67
QY 100 SOVALENCASAVADTRCGCKPGWFVEC---QVSQCVSPPFYCQCLDGCALHRHRLCLS 156
Db 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCIN-GTVH----LSCQ 117
QY 157 RRDTDCGTCCLPGFVEHGDGVCSTPTSLGSCPE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLRENEVCSC-----SNCKKSLECTKLC 153
RESULT 10
US-09-523-323-53
Sequence 53, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000C
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/142,657
EARLIER FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 60/124,041
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 09/252,656
EARLIER FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 60/075,409
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 60/013,923
EARLIER FILING DATE: 1996-03-22
EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 53
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
US-09-523-323-53
Query Match 17.7%; Score 200.5; DB 4; Length 154;

Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCOACDEQA 99
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGFTASENHLR-HCLSCSKCRKEM 67
Qy 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLTLC 156
Db 68 GQVEISCTVDRDTCVCGCRKNQYRHWSENLFCQ-----FNCSLCNLN-GTVH-----LSCQ 117

Qy 157 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 195
Db 118 EKQNTVCTCHAGFFLENECVSC-----SNCKSLECTKLC 153

RESULT 11
US-09-326-394-2
; Sequence 2, Application US/09326394
; Patent No. 6306820
; GENERAL INFORMATION:
; APPLICANT: Bendele, Alison M.
; APPLICANT: Sennello, Regina M.
; APPLICANT: Edwards, Carl K.
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/326,394
; APPLICATION NUMBER: US/09/326,394
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,587
; FILING DATE: 06-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,355
; FILING DATE: 23-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,315
; FILING DATE: 07-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/052,023
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zindrick, Thomas K.
; REGISTRATION NUMBER: 32,185
; REFERENCE/DOCKET NUMBER: A-430D
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-326-394-2

Query Match 17.7%; Score 200.5; DB 3; Length 161;
Best Local Similarity 29.8%; Pred. No. 3.7e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCOACDEQA 99

Db 11 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGFTASENHLR-HCLSCSKCRKEM 69
Qy 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLTLC 156
Db 70 GQVEISCTVDRDTCVCGCRKNQYRHWSENLFCQ-----FNCSLCNLN-GTVH-----LSCQ 119
Qy 157 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKSLECTKLC 155

RESULT 12
US-08-232-087A-10
; Sequence 10, Application US/08232087A
; Patent No. 5866372
; GENERAL INFORMATION:
; APPLICANT: Stein, Harald
; APPLICANT: Dtkop, Horst
; APPLICANT: Latza, Ute
; TITLE OF INVENTION: Lymphoid CD30-Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/232,087A
; APPLICATION NUMBER: US/08/232,087A
; FILING DATE: 08-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 756-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 154 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..154
; OTHER INFORMATION: /note= "TNFR1, see Fig. 5"
US-08-232-087A-10

Query Match 17.6%; Score 198.5; DB 2; Length 154;
Best Local Similarity 30.4%; Pred. No. 5.4e-11;
Matches 49; Conservative 23; Mismatches 68; Indels 21; Gaps 8;

Qy 40 HKKIGLFCRCGPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCOACDEQA 99
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECESGFTASENHLR-HCLSCSKCRKEM 67
Qy 100 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLTLC 156
Db 68 GQVEISCTVDRDTCVCGCRKNQYRHWSENLFCQ-----FNCSLCNLN-GTVHLSGQ---E 118
Qy 157 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 195


```
Db      119 KQNTVC-TCHAGFFLRENECVSC-----GNCKKSELETKLC 153  
:  
  
RESULT 13  
US-08-706-945D-129 ; Sequence 129, Application US/08706945D  
; Patent No. 6369027  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Lacey, David  
; APPLICANT: Calzone, Frank  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; FILE REFERENCE: A-378CIP  
; CURRENT APPLICATION NUMBER: US/08/706,945D  
; PRIOR FILING DATE: 1996-09-03  
; PRIOR APPLICATION NUMBER: 08/577,788  
; PRIOR FILING DATE: 1995-12-22  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 129  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-08-706-945D-129
```

```
Query Match          17.3%; Score 196; DB 3; Length 139;  
Best Local Similarity 31.5%; Pred.No. 8.2e-11;  
Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;
```

```
QY     40 HKKIGLFCCRCGPAGHYLKAPCTEPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 99  
       :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB     8 HPQNNSICCTKKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCRKM 66  
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

```
QY    100 SOVALENCSAVADTRCCCKGWFEVC---QVSQCIVSSPPFCQLDCGALHRHTRLICS 156  
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB    67 GOVEISSCTVDNRDTVCGCRKNQRHWSENLFQC----FNCSLCLN-GTVH----LSQQ 116  
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

```
QY    157 RRDTDGCTGLPGRFYEHGDDGVSC 179  
         :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB   117 EKONTVTCTCHAGFFLRENECVSC 139  
         :
```

```
RESULT 14  
US-09-513-007-4 ; Sequence 4, Application US/09513007  
; Patent No. 6406907  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, J. Michael  
; APPLICANT: Kehrl, Jr., Marcus  
; APPLICANT: Lee, Eun-Kyung  
; APPLICANT: Mwanga, Simon  
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1  
; TITLE OF INVENTION: AND METHODS OF USE  
; FILE REFERENCE: 08411-018001  
; CURRENT APPLICATION NUMBER: US/09/513,007  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 60/122,156  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; US-09-513-007-4
```

```
Query Match          16.9%; Score 191; DB 4; Length 181;  
Best Local Similarity 31.0%; Pred.No. 3.1e-10;  
Matches 48; Conservative 17; Mismatches 76; Indels 14; Gaps 6;
```

```
OY     40 HKKIGLFCCRCGPAGHYLKAPCTEPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 99
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:04:00 ; Search time 38 Seconds
(without alignments)
440.571 Million cell updates/sec

Title: US-10-081-280-6_COPY_25_198
Perfect score: 1038
Sequence: 1 QGGTRSPRCDGDFHKKIG.....CPTSTLGSPCRCAAVCGWR 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 87400

Minimum DB seq length: 0
Maximum DB seq length: 174

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	9.9	169	1 S18946	ultra high-sulfur
2	96.5	9.3	141	2 PC1294	trophozoite surfac
3	96	9.2	149	2 S58662	Fas-Delta-(4,7) pr
4	94.5	9.1	104	2 S50911	metallothionein-2
5	93.5	9.0	143	2 B21761	high cysteine chor
6	90	8.7	126	2 I46489	cysteine-rich hair
7	88	8.5	167	1 AG0369	ferredoxin-type pr
8	86	8.3	151	2 S60314	hair keratin cystei
9	84.5	8.1	168	2 S06570	finger protein (cl
10	83.5	8.0	131	1 KRGT3M	keratin high-sulfu
11	83.5	8.0	152	2 I47108	high-sulfur wool m
12	83.5	8.0	171	2 I48298	cellular nucleic a
13	83	8.0	170	2 A55499	zinc finger protei
14	83	8.0	170	2 I48297	cellular nucleic a
15	82.5	7.9	133	2 T20467	hypothetical prote
16	82	7.9	130	1 KRSH3A	keratin high-sulfu
17	81.5	7.9	164	2 T24272	hypothetical prote
18	80.5	7.8	163	2 F65072	hypothetical prote
19	80	7.7	157	2 G65156	Putative electron
20	80	7.7	160	2 T25185	hypothetical prote
21	79.5	7.7	157	2 F86032	hypothetical prote
22	79.5	7.7	157	2 H91185	hypothetical prote
23	79.5	7.7	168	1 B82430	iron-sulfur cluste
24	79	7.6	132	2 T20463	hypothetical prote
25	78.5	7.6	92	2 D37057	epithelial cell gl
26	78	7.5	79	2 E83378	probable metalloth
27	78	7.5	152	1 KRSHHC	keratin high-sulfu
28	78	7.5	152	2 I47111	keratin high-sulfu
29	78	7.5	155	2 B32669	vasotocin 2 / neur

ALIGNMENTS

RESULT 1

S18946
ultra high-sulfur keratin 1 - human
N:Alternate names: UHS keratin; ultra high-sulfur matrix protein
C:Species: Homo sapiens (man)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: S18946; B36686
R:Drabant, B.; Doenecke, D.
submitted to the EMBL Data Library, December 1991
A:Description: Nucleotide sequence of a Human high-sulphur keratin cDNA.
A:Reference number: S18946
A:Accession: S18946
A:Molecule type: mRNA
A:Residues: 1-169 <DRA>
A:Cross-references: UNIPROT:Q14564; EMBL:X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472
R:MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.
J. Cell Biol. 111, 2587-2600, 1990
A:Title: Structure and expression of genes for a class of cysteine-rich proteins of the c
A:Reference number: A36686; MUID:91115951; PMID:1703541
A:Accession: B36686
A:Molecule type: DNA
A:Residues: 1-39, 'Y', 41-169 <MAC>
A:Cross-references: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079
C:Genetics:
A:Gene: GDB:KRN1
A:Cross-references: GDB:i25257; OMIM:148021
A:Map position: 11q13-11q13
C:Superfamily: ultra-high-sulfur keratin
C:Keywords: hair; tandem repeat
F:7-15/Region: Ser-rich nonapeptide repeat
F:59-68/Region: Gly-rich decapeptide repeat
F:69-78/Region: Gly-rich decapeptide repeat
F:79-88/Region: Cys-rich decapeptide repeat
F:89-97/Region: Ser-rich nonapeptide repeat
F:98-107/Region: Cys-rich decapeptide repeat
F:108-117/Region: Cys-rich decapeptide repeat
F:118-126/Region: Ser-rich nonapeptide repeat
F:127-136/Region: Cys-rich decapeptide repeat
F:137-145/Region: Ser-rich nonapeptide repeat
F:146-155/Region: Cys-rich decapeptide repeat
F:156-165/Region: Cys-rich decapeptide repeat

Query Match '9.9%'; Score 103; DB 1; Length 169;

Best Local Similarity 25.3%; Pred. No. 0.58;

Matches 45; Conservative 6; Mismatches 71; Indels 56; Gaps 12;

QY 23 CCRCPAGHYLKAPCTEPCG--NSTCLVCPQDTFLAMENHFNSECARCQ-----ACD 72

Db 3 CC-GCSGG-----CGSSCGGCDSSCGSC-----GSGCRGGGSPSCAPVCCCK 43

QY 73 EQASQVALENCSAVADTRCG-C--KPGWFVFCQVSCVSSSPFFVC-----QPCLDCCGALH 124

Db 44 PVCCVPACSSCGKRGCGSGKGGCGSCGSCCKPCGCCSGSGSCCQCSC-- 101

QY 125 RHTRLLCSRRDTCGTCLPGFYEHGSG---CVS-----CPTSTLGS--CPCRCAAVC 171

Db 102 -----CRPYCQCSCCKPCPCSSSGSGSCCQSSCKPCPCSSSGSGSCCCKPC 153

RESULT 2

PC1294

trophozoite surface antigen - Giardia lamblia (strain Adelaide-1) (fragment)

C:Species: Giardia lamblia

C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004

C:Accession: PC1294

R:EtY, P.L.; Mayrhofer, G.

Gene 129, 257-262, 1993

A:Title: Two genes encoding homologous 70-kDa surface proteins are present within individual

A:Reference number: PC1294; MUID:93314970; PMID:8323510

A:Accession: PC1294

A:Molecule type: DNA

A:Residues: 1-141 <EXP>

C:Genetics: ts

A:Gene: ts

C:Keywords: surface antigen

Query Match 9.3%; Score 96.5; DB 2; Length 141;

Best Local Similarity 27.2%; Pred. No. 1.5;

Matches 41; Conservative 10; Mismatches 65; Indels 35; Gaps 9;

QY 42 GNSTCLVCPQDTFLAWHHNSECA-----RCQACDEQASQVALENCSSAVADT-----RCG 92

Db 3 GASYSCECATTT-----EYPQNGVCAPKASRATPTCNDSPIQNGV--CGTCADNYFKMNGG 56

QY 93 C-----KPCWFVECVQSVCS-SPFYCQPCLDGALHRRHRLLCGR-----RDTDCGT 140

Db 57 CYETVKYPKTV-----CISAPNGTCKAAGYKLDGSLTVCSEGCKCTSTSDCTT 110

QY 141 CLPGFYEHGDCVSCPTS--TLGSCPCRCAA 169

Db 111 CLDGVVKSASACTKDCSSCETCNGAATTCKA 141

RESULT 3

S58662

Fas-Delta-(4,7) protein - human

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: S58662; S57566

R:LiU, C.; Cheng, J.; Mountz, J.D.

Biochem. J. 310, 957-963, 1995

A:Title: Differential expression of human Fas mRNA species upon peripheral blood mononuclear

A:Reference number: S58662; MUID:96013198; PMID:7575433

A:Accession: S58662

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-149 <LIU>

A:Cross-references: UNIPROT:P25445

R:Schatzlein, C.E.

submitted to the EMBL Data Library, June 1995

A:Reference number: S57565

A:Accession: S57566

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-132 <SCH>

A:Cross-references: EMBL:X89101; NID:g887457; PID:g887458

C:Keywords: alternative splicing

Query Match 9.2%; Score 96; DB 2; Length 149;

Best Local Similarity 33.3%; Pred. No. 1.7;

Matches 18; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

QY 20 GLFCRCGCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWHHNSECARCQACDE 73

Db 56 GQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKRCRRCLCDE 109

RESULT 4

S50911

metallothionein-2 - Tetrahymena pigmentosa

C:Species: Tetrahymena pigmentosa

C:Date: 15-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: S50911

R:Piccinni, E.; Staudemann, W.; Albergoni, V.; de Gabrieli, R.; James, P.

Eur. J. Biochem. 226, 853-859, 1994

A:Title: Purification and primary structure of metallothioneins induced by cadmium in the

A:Reference number: S50911; MUID:95112850; PMID:7813475

A:Accession: S50911

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <PIC>

A:Cross-references: UNIPROT:P80394

C:Genetics:

A:Genetic code: SGC5

Query Match 9.1%; Score 94.5; DB 2; Length 104;

Best Local Similarity 34.3%; Pred. No. 1.8;

Matches 23; Conservative 8; Mismatches 29; Indels 7; Gaps 3;

QY 9 CDCAGDFHKIGLFCR---GCPAGHYLKAPCTEPCGNTCLVCPQDTFLAWHHNSE 64

Db 40 CTGTGEGCKTGCKCQCPAKSGCCGDKAKACCTDP--NSGC-CCSSKTNKCCDSTNKTE 96

QY 65 CARCOAC 71

Db 97 KTCCECC 103

RESULT 5

B21761

high cysteine chorion B 12 protein precursor - silkworm

C:Species: Bombyx mori (silkworm)

C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Jan-2000

C:Accession: B21761

R:Iatrou, K.; Tsicilou, S.G.; Kafatos, F.C.

Proc. Natl. Acad. Sci. U.S.A. 81, 4452-4456, 1984

A:Title: DNA sequence transfer between two high-cysteine chorion gene families in the sil

A:Reference number: A21761; MUID:84272653; PMID:6589605

A:Accession: B21761

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-143 <IAT>

C:Superfamily: chorion class A protein pc292

Query Match 9.0%; Score 93.5; DB 2; Length 143;

Best Local Similarity 20.7%; Pred. No. 2.6;

Matches 36; Conservative 8; Mismatches 61; Indels 59; Gaps 8;

QY 9 CDCAGDFHKIGLFCRCPAGHYLKAPCTEPCGNTCLVC-----PQDTFLAW 57

Db 24 CGC-----CCRGCGCG-----CGCGCGCCENFRVCSNSAAPTGLSICS 62

QY 58 ENHHNSCARCQACDEQASQVALENCSSAVADTRCGCKPGWFVECVQSQVSSSPFYCQPC 117

Db 63 ENRYKGDVVC---VCGEVPFLGTADVCGNMSCSGCGCID-----YCGGNGCVGITRSC 111

QY 118 LDCGALHRRHRLLCRRDTCGTCLPGFYEHGDCVSCPTSTLGCPCPCRCAAVC 171

Db 112 GCGCG-----GCGGC-----GCGCGG-----GCCGSCGRSC 139

RESULT 6

I46489

cysteine-rich hair keratin associated protein - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: I46489; S49201

R.Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A:Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A:Reference number: I46489; MUID:95228955; PMID:7536172
A:Accession: I46489
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-126 <POW>
A:Cross-references: UNIPROT:Q28707; EMBL:X80035; NID:g510540; PIDN:CAA56339.1; PID:g510540
A:Gene: KAP4L
C:Superfamily: ultra-high-sulfur keratin

Query Match 8.7%; Score 90; DB 2; Length 126;
Best Local Similarity 25.4%; Pred. No. 4.3;
Matches 43; Conservative 9; Mismatches 43; Indels 74; Gaps 15;
QY 11 CAGDPHKKIGLFCR-GCPAGHYLKAPCTEP-CGNSTCLVCPQDTFLAWENHNHSEACRC 68
DB 15 CQDPCQBS-CCRPSC-----CRPQCQPSCCRPTCCI-----SSCCRP 53
QY 69 QACDQASQVALENCASAVADTRCGCKPGWFVEQVSCVSSPFYCPQCLDCGALHRRHTR 128
DB 54 QCCQ-----SVCCQPTC-CRP-----SCYISSC-CRPTCCRP----- 83
QY 129 LLCRSR-----RDTDCGT-----CLPGFYEHGDCVSS--C-PTSTLGS 163
DB 84 -TCRPTCCRPSTCQTTCRTQCCRPSC-----CVSTCCRPCCSSGSC 125

RESULT 7
AG0369
ferredoxin-type protein NapF [imported] - Versinia pestis (strain CO92)
C:Species: Versinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG0369
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Versinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0369
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-167 <KUR>
A:Cross-references: UNIPROT:Q8ZCF1; GB:AL590842; PIDN:CAC92282.1; PID:g15980993; GSPDB:C
C:Genetics:
A:Gene: napF
C:Superfamily: ferredoxin protein NapF; ferredoxin 2 [4Fe-4S] homology

Query Match 8.5%; Score 88; DB 1; Length 167;
Best Local Similarity 23.2%; Pred. No. 7.1;
Matches 36; Conservative 18; Mismatches 47; Indels 54; Gaps 11;
QY 26 GCPAGHYLKAPCTEPCGNSTCLV-----CPQDTFLAWENHNHSEACRCQACDEQASQVALE 81
DB 38 GCTRCH-----ACVSACETGVLIAGSGFPIDF-----QRAECFQCAC-VQACEAAI- 85
QY 82 NCSAVADTRCGCKPGWFVEQVSCVSSPFYCPQCLD-CGALHRRHLLCSR----- 133
DB 86 -FTSVEQT-----AMQIKASISDRCLPVNVECRSCQDSC-----ETRAIKFRPLSGI 133
QY 134 -----RDTDCGTCLPGFYEHGDCVSCPTSTL 160
DB 134 AQPELDLPACTCGGACVFG-----CPVQAV 158

RESULT 8
S60314
hair keratin cysteine rich protein - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C:Accession: S60314
R:Frattini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.
J. Invest. Dermatol. 102, 178-185, 1994
A:Title: Dietary cysteine regulates the levels of mRNAs encoding a family of cysteine-rich proteins
A:Reference number: S60314; MUID:94149288; PMID:7508963
A:Accession: S60314
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-151 <FRA>
A:Cross-references: UNIPROT:Q28576; EMBL:X73462; NID:g512030; PIDN:CAA51841.1; PID:g512030
C:Superfamily: ultra-high-sulfur keratin

Query Match 8.3%; Score 86; DB 2; Length 151;
Best Local Similarity 24.8%; Pred. No. 9.4;
Matches 38; Conservative 14; Mismatches 61; Indels 40; Gaps 10;
QY 23 CCR-GCPAGHYLKAPCTEP-CGNSTCL--VCPQDTFLAWENHNHSEACRCQACDEQASQV 78
DB 24 CCRSCCQTTCCRTTCYRPSGCVSSCCRPICQPT-----CRPTCC----- 65
QY 79 ALENCASAVADTRCGCKPGWFVEQVSCVSS--SPFYCQP--CLDCGALHRRHLLCSR 134
DB 66 -ISSCYRPSCCRSSCGSSCY--RPTSCISSCCRPQCCQPVCCQPSGA-----RISSCCR 116
QY 135 DTDGCTCLPGFYEHGDCVSCPTSTLGSCTP 167
DB 117 PSCGSSC-----YRPSCLRPVGNRVSCHTTC 144

RESULT 9
S06570
finger protein (clone XlCGF42-1) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S06570
R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Posting, A.; Knoechel, J. Mol. Biol. 208, 639-659, 1989
A:Title: Second-order repeats in Xenopus laevis finger proteins.
A:Reference number: S05632; MUID:90040698; PMID:2509712
A:Accession: S06570
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-168 <NI2>
A:Cross-references: UNIPROT:P18720
C:Keywords: DNA binding; zinc finger

Query Match 8.1%; Score 84.5; DB 2; Length 168;
Best Local Similarity 23.3%; Pred. No. 13;
Matches 41; Conservative 13; Mismatches 77; Indels 45; Gaps 9;
QY 3 GTRSPRC-DCAGDFHKKIGL-----FCRCGCPAG-----HYLKAPCTEP 40
DB 2 GEKPYSCDCGCKFTRRWNLSEHRKSHGTQKRFCCSVCGKGFVSHQMSKSHVYRHTGK 61
QY 41 CGNSTCLVCPD--TFLAWENHNHNS-----ECARCQACDEQASQVALENCASAVADTRCGCK 94
DB 62 CICSECGKSFTHAGLRHQYHTGVKFPSCSECGKCFRRS-----GLTAHLRIHTGK 116
QY 95 PGWFVEQVSCVSSPFYCPQCLDCGALHRRHLLCSRRTDCGTCLPGFYEHGD 150
DB 117 PYTCTEC--GKC-----FTCRT-----DLARHLRIHTENKFTCSQCEKSFASHSD 160

RESULT 10
KRG73M
keratin high-sulfur matrix protein IIIA3, minor component - goat
N:Alternate names: M2.6 protein
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: B92978; A02840
R:Joubert, F. J.
J. S. Afr. Chem. Inst. 28, 250-263, 1975
A:Title: Studies on the high-sulphur proteins of reduced mohair. The isolation and the an

A:Reference number: A92978
A:Accession: B92978
A:Molecule type: protein
A:Residues: 1-131 <JOB>
A:Cross-references: UNIPROT:P02442
A:Experimental source: Angora breed
C:Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other proteins
C:Superfamily: keratin high-sulfur matrix protein IIIA
C:Keywords: duplication; hair

Query Match 8.0%; Score 83.5; DB 1; Length 131;
Best Local Similarity 22.8%; Pred. No. 13;
Matches 42; Conservative 5; Mismatches 46; Indels 91; Gaps 14;

QY 2 GGTSPRC---DCAGDFHKKIGLFCRCGCPAGHYLKAP-----CT-----EPCGNSTCLV 48
DB 16 GGLQPRCYRDPD-----CCRPVSCQTTVSRPTFVSRTRPFCRPRPVC-- 62

QY 49 CPQDTFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPGWFVECVSQVCS 108
DB 63 -----CDPCSLQ-----EGC-----CRP-----ITCCPTSC-- 83

QY 109 SSPFYCQCLDGGALHRRLLCSRDDTGGTCLPFGFYEHDGCVSCPTSTLGSC-PERC 167
DB 84 -QAVVCRPC--CWA-----TTC--CQP-----VSQCPCCRPTSCQPAPC 118

QY 168 AAVC 171
DB 119 RTTC 122

RESULT 11
147108
high-sulfur wool matrix protein B2C - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I47108
R:Warden, C.H.; Bickerstaffe, R.
Anim. Genet. 25, 407-415, 1994
A:Title: Polymorphism in two genes for B2 high sulfur proteins of wool.
A:Reference number: I47105; MUID:95209146; PMID:7695121
A:Accession: I47108
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-152 <ROG>
A:Cross-references: UNIPROT:Q29620; GB:L33888; NID:g499874; PIDN:AA801447.1; PID:g940358
C:Superfamily: keratin high-sulfur matrix protein IIIA

Query Match 8.0%; Score 83.5; DB 2; Length 152;
Best Local Similarity 22.0%; Pred. No. 14;
Matches 39; Conservative 15; Mismatches 68; Indels 55; Gaps 10;

QY 23 CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCDQASQVALEN 82
DB 3 CCSTSFSGFPPI-CPTAGTCGSSCC-----RSTCGTSCC--QPTSIQTS 44

QY 83 CSAVADTRCGCKPGWFVECV-----SQCVSSSPFYCQP-----CL----- 118
DB 45 CQPTCLQTSQCKTGCGIGSGYGVGSSGAVSRTWCRPDVGRVSLPPCCVSGCTS 104

QY 119 -DCGALHRRLLCSRDDTDCG--TCLPFGFYEHDGCVSCPTSTLGSCPERCA-AVC 171
DB 105 PSCCOLYYAQAACC--RFSYCGQSCRP-----ACCCQPTCTEPVCEPTCSQPIC 152

RESULT 12
148298
cellular nucleic acid binding protein clone 14 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48298; S19360
R:Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Te
Genomics 24, 14-19, 1994

A:Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identifier
A:Reference number: A55499; MUID:95203870; PMID:7896269
A:Accession: I48298
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-171 <RES>
A:Cross-references: UNIPROT:P53996; EMBL:Z11871; NID:g50474; PIDN:CAA77897.1; PID:g50475
C:Superfamily: cellular nucleic acid-binding protein

Query Match 8.0%; Score 83.5; DB 2; Length 171;
Best Local Similarity 26.8%; Pred. No. 15;
Matches 34; Conservative 13; Mismatches 59; Indels 21; Gaps 7;

QY 8 RDCAGDFHKKIGL---FCRCGCPAGHYLKAPCTEP-----CGNSTCLVCPQDTFLAWEN 58
DB 49 RCGSGHLAKDCDLQEDACYNCGRGGHIADCKEPREREQC-----CYNCGKPGHLARDC 104

QY 59 NHHNSECARCAQCDQASQVALENCASAVADTRCGCKPGWFVECVSQVSSSPFYCQPCL 118
DB 105 CDHADE-QKVCSCGEFGH--IQDKCTVKYCRCG-ETGHV-----AINCSKTSEVNCYRCG 156

QY 119 DCGALHR 125
DB 157 ESGHLAR 163

RESULT 13
A55499
zinc finger protein 9 - human
N:Alternate names: nucleic acid binding protein
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
C:Accession: A55499
R:Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Te
Genomics 24, 14-19, 1994
A:Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identifier
A:Reference number: A55499; MUID:95203870; PMID:7896269
A:Accession: A55499
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-170 <RES>
A:Cross-references: GB:L12693; NID:g292347; PIDN:AAA89198.1; PID:g292348
C:Genetics:
A:Gene: GDB:ZNF9
A:Cross-references: GDB:125342; OMIM:116955
A:Map position: 3q13.3-3q24
C:Superfamily: cellular nucleic acid-binding protein

Query Match 8.0%; Score 83; DB 2; Length 170;
Best Local Similarity 27.0%; Pred. No. 17;
Matches 34; Conservative 13; Mismatches 59; Indels 20; Gaps 7;

QY 8 RDCAGDFHKKIGL---FCRCGCPAGHYLKAPCTEP-----CGNSTCLVCPQDTFLAWEN 59
DB 49 RCGSGHLAKDCDLQEDACYNCGRGGHIADCKEPREREQC-----CYNCGKPGHLARDC 104

QY 60 NHHNSECARCAQCDQASQVALENCASAVADTRCGCKPGWFVECVSQVSSSPFYCQPCLD 119
DB 105 DHADE-QKVCSCGEFGH--IQDKCTVKYCRCG-ETGHV-----AINCSKTSEVNCYRCG 156

QY 120 CGALHR 125
DB 157 SGHLAR 162

RESULT 14
148297
cellular nucleic acid binding protein clone 6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48297; S19861; S19959
R:Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Te
Genomics 24, 14-19, 1994

Search completed: June 27, 2005, 14:19:24
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:05:01 ; Search time 173 Seconds
(without alignments)
515.039 Million cell updates/sec

Title: US-10-081-280-6_COPY_25_198

Perfect score: 1038

Sequence: 1 QGTRSPRCAGDFHKKIG.....CPTSTLGCSPERCAAVCGWR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 561438

Minimum DB seq length: 0

Maximum DB seq length: 174

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	165.5	15.9	150	2 Q9R230	Q9c230 rattus norv
2	161.5	15.6	130	2 Q8MJ20	Q8mj20 macaca mula
3	146.5	14.1	146	2 Q7Z2Y4	Q7zzy4 gallus gall
4	135	13.0	147	2 Q8SQ52	Q8sq52 felis silve
5	133.5	12.9	124	2 Q8SQ51	Q8sq51 felis silve
6	127.5	12.3	169	2 Q8JKE0	Q8jke0 rattus norv
7	126.5	12.2	65	2 Q8SQ49	Q8sq49 felis silve
8	125	12.0	110	2 Q9BIR2	Q9bir2 paramacium
9	124	11.9	110	2 Q9BIR3	Q9bir3 paramacium
10	124	11.9	117	2 Q6VZRI	Q6vzri canarypox v
11	123	11.8	167	2 Q8BDC5	Q8bdc5 human cytom
12	121.5	11.7	172	2 Q8F2H9	Q8f2h9 homo sapien
13	119	11.5	151	2 Q8F2H9	Q8f2h9 homo sapien
14	111.5	10.7	166	2 Q8BDC6	Q8bdc6 human cytom
15	109	10.5	118	2 Q8WTI6	Q8wti6 drosophila
16	108.5	10.5	171	2 Q7TFH9	Q7tfh9 rhesus cyto
17	106.5	10.3	174	2 Q9N2N0	Q9n2n0 bombyx mori
18	105	10.1	137	2 Q6ITV8	Q6itv8 branchiost
19	104.5	10.1	167	2 Q9DJL2	Q9dj12 cowpox viru
20	104	10.0	169	1 KRUA HUMAN	P26371 homo sapien
21	103.5	10.0	167	2 Q72762	Q72762 cowpox viru
22	103.5	10.0	167	2 Q8UYL3	Q8uy13 vaccinia vi
23	103	9.9	169	2 Q14564	Q14564 homo sapien
24	102.5	9.9	167	2 Q8BDC3	Q8bdc3 human cytom
25	100.5	9.7	166	2 Q8BDC4	Q8bdc4 human cytom
26	100	9.6	90	2 Q6SC66	Q6sc66 camelpox vi
27	98.5	9.5	167	2 Q8BDC7	Q8bdc7 human cytom
28	98	9.4	170	2 Q9D548	Q9d548 mus musculu
29	97.5	9.4	167	2 Q701N3	Q701n3 homo sapien
30	97	9.3	142	2 Q919J2	Q919j2 xenopus lae
31	97	9.3	148	2 O57093	O57093 cowpox viru

32 97 9.3 173 2 Q6ISF6 Q6isf6 homo sapien
33 96.5 9.3 168 2 Q9D732 Q9d732 mus musculu
34 96 9.2 174 1 KR92 HUMAN K92yq4 homo sapien
35 94.5 9.1 107 1 MT1_TETPI P80394 tetrahymena
36 94.5 9.1 107 1 MT1_TETTH O8t6b3 tetrahymena
37 94 9.1 143 2 Q9I3J3 O9i9j3 xenopus lae
38 93.5 9.0 107 1 MT1_TETPY O97388 tetrahymena
39 92.5 8.9 160 2 O83022 O83022 rhodobacter
40 92.5 8.9 160 2 Q9RAD6 Q9rad6 rhodobacter
41 92 8.9 155 2 Q6Y1L9 Q6y1l9 drosophila
42 92 8.9 165 2 O6L8G8 O6l8g8 homo sapien
43 91.5 8.8 129 2 Q6L8G9 O6l8g9 homo sapien
44 91.5 8.8 136 1 KR42 HUMAN K42y25 homo sapien
45 91.5 8.8 139 2 Q8RYZ5 Q8ryz5 oryza sativ

ALIGNMENTS

RESULT 1
Q9R230 ID Q9R230 PRELIMINARY; PRT; 150 AA.
AC Q9R230;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fas receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Corpus luteum;
RA Lareu R.R., Dharmarajan A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104034; AAD20221.1; -.
DR HSSP; Q92956; IJMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00505; TNFR_NGFR_2; 1.
KW Receptor.
FT NON TER 1 150
FT NON TER 150 150
SQ SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;

Query Match 15.9%; Score 165.5; DB 2; Length 150;

Best Local Similarity 30.8%; Pred. No. 1.7e-06;

Matches 32; Conservative 13; Mismatches 52; Indels 7; Gaps 2;

Qy 18 KIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNHSECARCQACDEQASQ 77
Db 45 QVGFPCQCPQPGERKVKDCTTSGAPTCHPCTGEEYDRKHYSKRCRCACFCDGHGL 104
Qy 78 VALENCASAVADTRCGCKPGFVEQCVSSSPFYCQPCILDCG 121
Db 105 EVELNCTRTQTKCRKENFY--CNASLC-----DHCYHCTSCG 141

RESULT 2

Q8MJ20 ID Q8MJ20 PRELIMINARY; PRT; 130 AA.
AC Q8MJ20
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fas receptor CD95 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnault D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530075; AAM95635.1; -.
DR HSSP; O14763; 1DU3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR Pfam; PF00020; TNFR_C6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14814 MW; 91542C61323F3C27 CRC64;

Query Match 15.6%; Score 161.5; DB 2; Length 130;
Best Local Similarity 31.7%; Pred. No. 3.3e-06;
Matches 32; Conservative 12; Mismatches 50; Indels 7; Gaps 1;

QY 20 GLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVA 79
DB 22 GQFCRNPCPPGERKARDCTVNEDEPDCVPCQEGKEYTDKGFHSKRCRLCDGHEGLEV 81
QY 80 LENCASVADTRCGCKPGWFCVQSVSSSFFYCPCLDC 120
DB 82 EINCTRTQNTKCRCKPNFF-----CNSAVCEHCDPCTKC 115

RESULT 3
ID Q7ZZY4 PRELIMINARY; PRT; 146 AA.
AC Q7ZZY4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Osteoprotegerin (Fragment).
GN Name=OPG;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22760275; PubMed=12878204; DOI=10.1016/S0006-291X(03)01304-4;
RA Bridgham J.T., Johnson A.L.;
RT "Characterization of chicken TNFR superfamily decoy receptors, Dcr3
RT and osteoprotegerin."
RL Biochem. Biophys. Res. Commun. 307:956-961(2003).
DR EMBL; AY251407; AAP03890.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR006209; EGF-like.
DR Pfam; PF00020; TNFR_C6; 2.
DR
```

```
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16487 MW; 1C9B64FE3A0FC2DF CRC64;

Query Match 14.1%; Score 146.5; DB 2; Length 146;
Best Local Similarity 28.3%; Pred. No. 6.6e-05;
Matches 39; Conservative 13; Mismatches 49; Indels 37; Gaps 7;

QY 24 CRGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNSECARCOA-CDEQASQVALEN 82
DB 41 CNQCPGSGYVYKHCT-AASTVTCAPCP-DQYAYADWNSNDECCQVCSAVCKE--LQYIKQE 96
QY 83 CSAVADTRCGCKPGWFCVQSVSSSFFYCPCLDCGALHRRHRLLCRRDTRDC---- 138
DB 97 CTSTQDRVCEICIGWYLELF-----CL-----KHTECPPGF 128
QY 139 GTCLPGFYEHGDCVSCP 156
DB 129 GVAQGPPESDTVCFCCP 146

RESULT 4
ID Q8SQ52 PRELIMINARY; PRT; 147 AA.
AC Q8SQ52;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fas (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
RT cells."
RL Eur. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072009; BAB86798.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR Pfam; PF00020; TNFR_C6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON_TER 1 1
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;

Query Match 13.0%; Score 135; DB 2; Length 147;
Best Local Similarity 27.4%; Pred. No. 0.00062;
Matches 32; Conservative 15; Mismatches 32; Indels 38; Gaps 6;

QY 59 NHNSECARCOACDEQASQVALENCSAVADTRCGCKPGWFCVQSVSSSFFYCPCLC 118
DB 10 SHFSPRCRCKICDEEHGLEVEKNCTRTQNTKCRCKSNFF--CNVSQC-----DHCNFCM 62
QY 119 DCGALHRRHRLLCRRDTRDCGCLPGFYEHG--DGCVCSTPTSLGSCPCERCAAVCGW 173
DB 63 MC-----EHGILENCT--FTSNT-KCKQSSSSKLLW 90
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RESULT 5
Q8SQ51 PRELIMINARY; PRT; 124 AA.
AC Q8SQ51;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Fas delta6 (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells";
RL Euk. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072010; BAB86799.1; -.
DR HSSP; O14763; 1DQG.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 124 AA; 14319 MW; 15A7DF058D79942 CRC64;

Query Match 12.9%; Score 133.5; DB 2; Length 124;
Best Local Similarity 29.4%; Pred. No. 0.0072;
Matches 30; Conservative 12; Mismatches 23; Indels 37; Gaps 5;

Qy 59 NHNSECARQCQACDQASQVALENCASAVADTCGCKPGWFCVQSVSSPFYCPCL 118
Db 10 SHPSRCRRCKICDEHGLEVEKNKTRQNTKCRCKSNFF--CNVSQC-----DHCNFCM 62
Qy 119 DCGALHRLRLCLSRDTCGTCPLGFEYHG--DGVSCPTSS 158
Db 63 MC-----EHGLENC--PTS 76

RESULT 6
Q9JKE0 PRELIMINARY; PRT; 169 AA.
AC Q9JKE0;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE R40 protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
EX MEDLINE=99330195; PubMed=10403401; DOI=10.1016/S0014-5793(99)00683-3;
RA Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
RT "Cytokine-inducible CD40 gene expression in vascular smooth muscle
cells is mediated by nuclear factor kappaB and signal transducer and
activator of transcription-1.";
RL FEBS Lett. 453:191-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
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RA Krzesz R., Hecker M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Smooth muscle;
RA Gao D., Hecker M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DE EMBL; AF241231; AAF43717.2; -.
DR HSSP; Q92956; 1JMA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; Ribosomal_S2.
DR Pfam; PF00020; TNFR_c6; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_3.
DR PROSITE; PS00652; RIBOSOMAL_S2_1; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
FT NON TER 169
SQ SEQUENCE 169 AA; 18525 MW; F199D91EFA224A26 CRC64;

Query Match 12.3%; Score 127.5; DB 2; Length 169;
Best Local Similarity 29.7%; Pred. No. 0.003;
Matches 44; Conservative 14; Mismatches 69; Indels 21; Gaps 8;

Qy 8 RDCAGDFHKKIGLFCRCGCPAGHYLKAPCTPCGNCSTCLVCPQDTFLAWNHNS--C 65
Db 22 QCVTCSDKQYLQGGECDCDLCQGNRLVSHCT-ALEKTCQCPDSEGFSA---HWNREIRC 77
Qy 66 ARCAQACD-EQASQVALENCASAVADTCGCKPGWFCVQSVSSPFYCPCLD---CG 121
Db 78 HQHRHCELNLQGLVKKEG-TAVSDTVCTCKEG-----QHCASKE---CETCAQHRFCG 126
Qy 122 ALHRLRLCLSRDTCGTCPLGFEYHG 149
Db 127 PGFGVQMATETDTVCQPCPVGFFSNG 154

RESULT 7
Q8SQ49 PRELIMINARY; PRT; 65 AA.
AC Q8SQ49;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Fas delta 5 delta 6 (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
RT "Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells";
RL Euk. J. Immunogenet. 31:159-166(2004).
DR EMBL; AB072012; BAB86801.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008063; Fas_receptor.
DR Pfam; PF00020; TNFR_c6; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_1.
DR PROSITE; PS00650; TNFR_NGFR_2; 1.
```

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FT NON TER 1
SQ SEQUENCE 65 AA; 7670 MW; A557395A3D527417 CRC64;

Query Match 12.2%; Score 126.5; DB 2; Length 65;
Best Local Similarity 36.7%; Pred. No. 0.0016;
Matches 22; Conservative 11; Mismatches 20; Indels 7; Gaps 2;

Qy 59 NHHNSECARCOACDEQASQVALENCNSAVADTRCGCKPGWFEVCQVSSSPFYCOPCL 118
Db 10 SHFSRCRRCKICDEEHGLEVEKNTQNTQNTCKCKSNFF--CNVSC-----DHCMPCM 62

RESULT 8
ID Q9BIR2 PRELIMINARY; PRT; 110 AA.
AC Q9BIR2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Furin-like protein (Fragment).
GN Name=fur;
OS Paramesidium aurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramesidium.
OX NCBI_TaxID=5889;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2998-axenic;
RA Wyroba E., Wlejak J., Surmacz L.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF351195; AAK27160.1; -.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac. recept.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
FT NON TER 1
FT NON TER 110
SQ SEQUENCE 110 AA; 11810 MW; 449E0D07D8BB0A91 CRC64;

Query Match 12.0%; Score 125; DB 2; Length 110;
Best Local Similarity 22.4%; Pred. No. 0.0034;
Matches 35; Conservative 17; Mismatches 52; Indels 52; Gaps 7;

Qy 8 RDCAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSCAR 67
Db 5 KCICSSNYISQLSLVCRAC-----ISPCLECLDDA--LALPAD-----GTQCVT 47

Qy 68 CQACDEQASQVALENCNSAVADTRCGCKPGWFEVCQVSSSPFYCOPCLDCGALHRT 127
Db 48 CQP-----GLNRIIDNNVNNKNCCLDGYETTGVLACTQCSP-----PCYDC----- 88

Qy 128 RLLCSRRDTCGTCLPGFYEHGDCVSCPTSTLGSC 163
Db 89 -----ADNGT-----GAECTTCPPGTFTLC 108

RESULT 9
ID Q9BIR3 PRELIMINARY; PRT; 110 AA.
AC Q9BIR3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Furin-like protein (Fragment).
GN Name=fur;
OS Paramesidium aurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramesidium.
OX NCBI_TaxID=5889;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2998-axenic;
RA Wyroba E., Wlejak J., Surmacz L.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
FT NON TER 1
FT NON TER 110
SQ SEQUENCE 110 AA; 11810 MW; 449E0D07D8BB0A91 CRC64;

Query Match 12.0%; Score 125; DB 2; Length 110;
Best Local Similarity 22.4%; Pred. No. 0.0034;
Matches 35; Conservative 17; Mismatches 52; Indels 52; Gaps 7;

Qy 8 RDCAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSCAR 67
Db 5 KCICSSNYISQLSLVCRAC-----ISPCLECLDDA--LALPAD-----GTQCVT 47

Qy 68 CQACDEQASQVALENCNSAVADTRCGCKPGWFEVCQVSSSPFYCOPCLDCGALHRT 127
Db 48 CQP-----GLNRIIDNNVNNKNCCLDGYETTGVLACTQCSP-----PCYDC----- 88

Qy 128 RLLCSRRDTCGTCLPGFYEHGDCVSCPTSTLGSC 163
Db 89 -----ADNGT-----GAECTTCPPGTFTLC 108

RESULT 10
ID Q6VZR1 PRELIMINARY; PRT; 117 AA.
AC Q6VZR1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CNPV086 TNFR-like protein.
GN Name=CNPV086;
OS Canarypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=44088;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC VR-111;
RX PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of canarypox virus.";
RL J. Virol. 78:353-366(2004).
DR EMBL; AY318871; AAR83432.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 117 AA; 13113 MW; 06E99CAB6A41135A CRC64;

Query Match 11.9%; Score 124; DB 2; Length 117;
Best Local Similarity 27.8%; Pred. No. 0.0043;
Matches 27; Conservative 20; Mismatches 46; Indels 4; Gaps 4;

Qy 12 AGDFHKKI-GLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSCARCOA 70
Db 24 ASTYRSKINSLLICDMCPGYYKNKDCST-TSITICLPCGEGEYATY-NNSLTCKIRCKD 81

Qy 71 CDEQASQVALENCNSAVADTRCGCKPGWFEVCQVSSSPFYCOPCLDCGALHRT 107
Db 82 CYBENEKI-FKPCNSTSDTICTCIDGYTKDFTDSCI 117

RESULT 11
ID Q8BDC5 PRELIMINARY; PRT; 167 AA.
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AC Q8BDC5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ULI44 (Fragment)
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=224242165; PubMed=12355354;
RA Arav-Boger R., Willoughby R.E., Pass R.P., Zong J.C., Jang W.J.,
RA Alencor D., Hayward G.S.;
RT "Polymorphisms of the cytomegalovirus (CMV)-encoded tumor necrosis
RT factor-alpha and beta-chemokine receptors in congenital CMV disease.";
RL J. Infect. Dis. 186:1057-1064 (2002).
DR EMBL; AF498088; AAN37947.1; -.
DR HSP; Q92956; IJWA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
FT NON TER 167
SQ SEQUENCE 167 AA; 18339 MW; C2495E13230E9616 CRC64;

Query Match 11.8%; Score 123; DB 2; Length 167;
Best Local Similarity 32.3%; Pred. No. 0.0072;
Matches 30; Conservative 16; Mismatches 35; Indels 12; Gaps 6;

D5 2 GGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHH 61
D6 18 GSGKM----CKPD-EVKLGNQCPCGSGQKVKVCTENSG-ITCLCPNGTYLT--CLY 69
D7 62 NSECARQACDEQASQVALENCASVADTRCGCK 94
D8 70 N--CTNCTQCND--TQITVRNCTSTNTICASK 98

QY 62 NSECARQACDEQASQVALENCASVADTRCGCK 94
DB 70 N--CTNCTQCND--TQITVRNCTSTNTICASK 98

RESULT 12
Q91IR0 PRELIMINARY; PRT; 172 AA.
AC Q91IR0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ULI44 protein.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RA He R., Ruan Q.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF382031; AAK60563.1; -.
DR HSP; Q92956; IJWA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 172 AA; 18911 MW; 9C9774EE9A07334C CRC64;

Query Match 11.7%; Score 121.5; DB 2; Length 172;
Best Local Similarity 33.8%; Pred. No. 0.0098;
Matches 26; Conservative 14; Mismatches 30; Indels 7; Gaps 4;

QY 18 KIGLFCRCGCPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHHNSECARQACDEQASQ 77
DB 29 KLGNCQPCPGSGQKVKVCTENSG-ITCLCPNGTYLT--GLYN--CTNCTQCND--TQ 81
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```
QY 78 VALENCASVADTRCGCK 94
DB 82 ITVRNCTSTNTVCASK 98

RESULT 13
Q6P2H9 PRELIMINARY; PRT; 151 AA.
AC Q6P2H9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE TNFRSF5 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064518; AAH64518.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007145; P:signal transduction; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 1.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 151 AA; 17079 MW; EBAA27CE7592172B CRC64;
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Query Match 11.5%; Score 119; DB 2; Length 151;
Best Local Similarity 27.8%; Pred. No. 0.014;
Matches 35; Conservative 13; Mismatches 42; Indels 36; Gaps 8;

QY 23 CCRGCPAGHYLKAPCTPCGNGSTCLVCPQDTFLAW--ENHNSECARQACDEQASQVA 79
DB 37 CCSLCQPGQKLVSDCTE-FTETCLPCGSEFDTWNRETHFHQH----KYCDPNLGLRV 91
QY 80 LENCASVADTRCGCKPGWFEVCQVSSPFFYQCPCLDCGALHRRHLLCSRDDTCG 139
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Db 92 QOKGTSETDTICTCEGW-----HCTSEA---CESCV-----LHR----- 123

Qy 140 TCLPGF 145

Db 124 SCSPGF 129

RESULT 14

Q8BDC6 ID Q8BDC6 PRELIMINARY; PRT; 166 AA.

AC Q8BDC6;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE UL144 (Fragment).

OS Human cytomegalovirus.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Betaherpesvirinae; Cytomegalovirus.

OX NCBI_TaxID=10359;

RN [1]

RP SEQUENCE FROM N.A. PubMed=12355354;

RX MEDLINE=22424165; Willoughby R.E., Pass R.F., Zong J.C., Jang W.J., Arav-Boger R., Hayward G.S.;

RA Alcendor D.,

RA "Polymorphisms of the cytomegalovirus (CMV)-encoded tumor necrosis factor-alpha and beta-chemokine receptors in congenital CMV disease.";

RT J. Infect. Dis. 186:1057-1064(2002).

RL EMBL; AF498087; AAN37946.1; -.

DR HSSP; Q92956; 1JMA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR001368; TNFR.c6.

DR Pfam; PF00020; TNFR.c6; 1.

DR SMART; SM00208; TNFR; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.

DR PROSITE; PS00500; TNFR_NGFR_2; 1.

FT NON TER 166 166

SQ SEQUENCE 166 AA; 18411 MW; 193D55AE19E046FA CRC64;

Query Match 10.7%; Score 111.5; DB 2; Length 166;

Best Local Similarity 28.6%; Pred. No. 0.066;

Matches 22; Conservative 20; Mismatches 28; Indels 7; Gaps 4;

Qy 18 KIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWNHHNSCARCQACDEQASQ 77

Db 29 QLGNQCCPPCKQGYRVTCQCTQ-YTSITCTLCPNGTYS--GLYN--CTNCTCND--TE 81

Qy 78 VALENCASAVADTRCGCK 94

Db 82 VTRNCTSTNNTVCASK 98

RESULT 15

Q8WTI6 ID Q8WTI6 PRELIMINARY; PRT; 118 AA.

AC Q8WTI6;

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE PFAIRE-interacting factor 2 (CG31483-PA).

GN Name=pf2; Synonyms=PIF-2; ORFNames=CG31483;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22667250; PubMed=12782278; DOI=10.1016/S0925-4773(03)00019-4;

RA Rascle A., Stowers R.S., Garza D., Lepesant J.-A., Hogness D.S., "L63, the Drosophila PFAIRE, interacts with two novel proteins unrelated to cyclins.";

RT Mech. Dev. 120:617-628(2003).

RL

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;

RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam K.A., Jalali M., Kalush K., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RA "The genome sequence of Drosophila melanogaster.";

RT Science 287:2185-2195(2000).

RL [3]

RN SEQUENCE FROM N.A.

RP MEDLINE=22426065; PubMed=12537568;

RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R., Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [4]

RN SEQUENCE FROM N.A.

RP MEDLINE=22426070; PubMed=12537573;

RX Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [5]

RN SEQUENCE FROM N.A.

RP MEDLINE=22426069; PubMed=12537572;

RX Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

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RT systematic review."
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF273708; AAL35411.1; -
DR EMBL; AE003674; AAF54113.3; -
DR HSP; F21860; IM68.
DR FlyBase; FEGn0046873; Pif2.
DR PROSITE; PS01208; VMFC_1; UNKNOWN_1.
SQ SEQUENCE 118 AA; 11566 MW; AF6FD15A61FF5C81 CRC64;

Query Match      10.5%; Score 109; DB 2; Length 118;
Best Local Similarity 23.8%; Pred. No. 0.08;
Matches 41; Conservative 3; Mismatches 62; Indels 66; Gaps 10;

Qy      6  SPPRC-DCAGDFHKKIIGLFCCRGCPCAGHYLKAPCTEPCGNSICLVCPQDTFLAWENHHNSE 64
Db      3  SPPCGSCCGP-----CCSPC-----CSPCCPPCCNDCCGSC----- 33

Qy     65  CARCQACDEQASQVALENCASAVADTRCG--CKPGWFVECVQSVSSPFYQCPCLDCGA 122
Db     34  ---CSPC-----CGPCCSPCCGCGCGSP-----CCSPCCTPCTCCTPCCKG-- 72

Qy    123  LHRHTRLCSRRDTCGT--CLPGFYEHDGCVSCPTSLGSCPERCAAVCG 172
Db     73  ----CTPCCVPCCTPCCTPCTP-----CTPCCSPCCGCGCCSPCCSPCG 113

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Job time : 175 secs

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OM protein - protein search, using sw model

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Title: US-10-081-280-6_COPY_25_198

Perfect score: 1038

Sequence: 1 QGTRSPRCAGDFHKKIG.....CPTSTLSCSPERCAAVCGWR 174

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1382563

Minimum DB seq length: 0
Maximum DB seq length: 174

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206.5	19.9	161	6 ABR62365	Abf62365 Tumour ne
2	200.5	19.3	154	3 AAY94711	Aay94711 Tumour ne
3	200.5	19.3	154	6 ADA49698	Ada49698 Extracell
4	200.5	19.3	154	7 ADL17741	Adl17741 Human tum
5	200.5	19.3	154	8 ADJ56814	Adj56814 Human TNF
6	200.5	19.3	161	2 ABG74752	Abg74752 Human TNF
7	200.5	19.3	161	2 AAR27496	Aar27496 Native 30
8	200.5	19.3	161	2 AAWS9664	AAWS9664 Human sol
9	200.5	19.3	161	2 AAW52267	Aaw52267 Soluble t
10	200.5	19.3	161	2 AAW89233	Aaw89233 Tumour ne
11	200.5	19.3	161	4 AAB37676	Abf37676 Human 30
12	200.5	19.3	161	6 ABR62363	Abf62363 Tumour ne
13	200.5	19.3	161	6 ADA20577	Ada20577 Human 30k
14	200.5	19.3	161	6 ADA20579	Ada20579 Human 30k
15	200.5	19.3	161	8 ADH78698	Adh78698 Human tum
16	198.5	19.1	162	5 AAM48058	Aam48058 Human TNF
17	197.5	19.0	161	6 ABR62364	Abf62364 Tumour ne
18	197	19.0	32	4 AAB84943	Aab84943 Human TR3
19	196	18.9	139	4 AAB66977	Abf66977 Peptide:
20	196	18.9	139	5 ABG71825	Abg71825 Wild type
21	196	18.9	139	8 ADM28814	Adm28814 Human TNF
22	190	18.3	32	8 ADH50950	Adh50950 Altered T
23	182	17.5	148	6 ABU60689	Abu60689 Human mat
24	182	17.5	155	6 ABU60676	Abu60676 Human mat
25	182	17.5	159	6 ABU60683	Abu60683 Human mat

26	181.5	17.5	161	7 ADL17744	Adl17744 Human TRA
27	181.5	17.5	161	8 ADJ56817	Adj56817 Human TR2
28	170.5	16.4	159	2 AAR24083	Aar24083 Truncated
29	165.5	15.9	169	2 AAR78612	Aar78612 Plasmid f
30	165.5	15.9	170	3 AAB36228	Aab36228 Rat Fas r
31	165	15.9	125	4 AAB37675	Aab37675 Human 30
32	164.5	15.8	148	8 ADM46624	Adm46624 Mouse 7F4
33	162.5	15.7	119	6 ADA49701	Ada49701 Extracell
34	162.5	15.7	144	2 AAW50286	Aaw50286 Human Fas
35	162.5	15.7	159	2 AAW50288	Aaw50288 Human Fas
36	162.5	15.7	167	6 ADA49708	Ada49708 Extracell
37	162.5	15.7	173	3 AAB36229	Aab36229 Human Fas
38	161	15.5	168	2 AAR24084	Aar24084 Truncated
39	155.5	15.0	133	7 ABW02714	Abw02714 Mouse tms
40	155.5	15.0	133	8 ADJ45750	Adj45750 Murine tm
41	152.5	14.7	158	2 AAR24081	Aar24081 Truncated
42	149.5	14.4	110	2 AAW52268	Aaw52268 Truncated
43	147.5	14.2	117	8 ADF57549	Adf57549 Mouse ymk
44	147	14.2	101	2 AAW52276	Aaw52276 Truncated
45	147	14.2	101	2 AAW89238	Aaw89238 Protein S

ALIGNMENTS

RESULT 1
ABR62365
ID ABR62365 standard; protein, 161 AA.
XX ABR62365;
AC
XX
DT 22-SEP-2003 (first entry)
XX
DE Tumour necrosis factor receptor extracellular domain H23P mutant.
XX
KW Tumour necrosis factor; receptor; TNFRp; proline; protein engineering;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 23 /note= "wild-type His substituted by Pro"
FT Misc-difference 46 /note= "wild-type Ser substituted by Ile"
XX
XX WO2003046160-A2.
XX
PD 05-JUN-2003.
XX
PF 21-NOV-2002; 2002WO-EP013059.
XX
PR 30-NOV-2001; 2001US-0340648P.
XX
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Brondyk W, Jiang X, Schweickhardt RL;
XX
DR WPI; 2003-523245/49.
XX
CC Increasing expression of a protein, comprises substituting at least one codon in the polynucleotide encoding the protein, for a codon encoding proline.
XX
PS Example 2; Page; 53pp; English.
XX
CC This is the protein sequence of a mutated extracellular domain of the p55 tumour necrosis factor receptor (TNFRp) in which a Pro residue
CC substitutes the native His-34 residue (residue 23 in the present
CC sequence) and an Ile residue substitutes the native Ser-57 residue
CC (residue 46 of the present sequence). Screening of TNFRp mutant clones
CC using a yeast display system yielded a clone that showed a higher

expression level in yeast than did a wild-type TNFR1 clone. The encoded polypeptide contained these 2 amino acid substitutions. The introduction of proline residues may assist the polypeptide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher yield of correctly folded proteins in yeast or mammalian host cells. The invention therefore provides methods of increasing protein expression levels by substituting an amino acid residue with proline, where the substitution occurs within 15 (preferably within 10, and especially within 5) amino acids of a cysteine residue. Note: the present sequence is not shown in the specification but is derived from the TNFR1 sequence given in figure 4 (see ABR62363)

XX Sequence 161 AA;

Query Match 19.9%; Score 206.5; DB 6; Length 161;

Best Local Similarity 30.4%; Pred. No. 6.2e-08;

Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDQOA 75
Db 11 HPQNNISICTCKPKGTLYNDPCPGQDTCRECEISFTASENHLR-HCLSCSKCRKEM 69
Qy 76 SQVALENCNSAVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132
Db 70 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 119
Qy 133 RRDTDCGTCPLGFVEHGDGCVSCPTSTLGSCE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155

RESULT 2

AA94711

ID AA94711 standard; protein; 154 AA.

AC AA94711;

DT 29-JAN-2001 (first entry)

DE Tumour necrosis factor receptor (TNFR) domain of TNFR-1.

XX Tumour necrosis factor receptor related protein; TR2; human; cancer;
KW chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
KW severely combined immunodeficiency; apoptosis inhibition;
KW Alzheimer's disease; Parkinson's disease; Crohn's disease.

XX Homo sapiens.

XX WO2000056405-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-US007521.

XX 22-MAR-1999; 99US-0125683P.

XX 26-MAR-1999; 99US-0126522P.

XX 20-MAY-1999; 99US-0135169P.

XX 06-AUG-1999; 99US-0147383P.

XX (NIJ//) NI J.

XX (ROSE//) ROSEN C A.

XX (GENTZ//) GENTZ R L.

XX Ni J, Rosen CA, Gentz RL;

XX WPI; 2000-594519/56.

XX Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
PT and its two splice variants, useful for treating arthritis or
PT inflammation, cancer (such as follicular lymphomas) and immunodeficiency
PT disorders.

XX Disclosure; Fig 16; 373pp; English.
PS This invention relates to an isolated nucleic acid molecule encoding a
CC human tumour necrosis factor (TNF)-receptor related protein TR2. Included
CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
CC member of the TNFR superfamily. The invention includes a method for the
CC treatment of arthritis or inflammation using an antibody directed against
CC a fragment of the TR2 protein. TR2 its agonists, antagonists and
CC antibodies exhibit cytostatic, dermatological, antianemic,
CC immunosuppressive, anti-allergic, antiarthritic, antiasthmatic,
CC anti-inflammatory, neuroprotective, nootropic, antiparkinsonian, and
CC cerebroprotective activity. The methods are useful for treating arthritis
CC mutations, cardiac tumors, pancreatic, breast, or prostate cancer, an
CC immunodeficiency or for enhancing an in vivo leukocyte response to an
CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
CC inflammatory myopathies) and immunodeficiency disorders (such as severely
CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
CC disorder, or Nezelof syndrome-combined immunodeficiency with Igs). TR2,
CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
CC antagonists are useful for treating or preventing autoimmune diseases and
CC inhibit the growth, progression and/or metastasis of cancers. They are
CC also used to activate, differentiate or proliferate cancerous cells or
CC tissues, and can be used to treat diseases associated with increased cell
CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
CC as sources for generating antibodies, as molecular weight markers. This
CC sequence represents the tumour necrosis factor receptor (TNFR) domain of
CC the human TNFR-1 protein. The sequence was used in the characterisation
CC of the TR2 receptor protein of the invention

XX Sequence 154 AA;

Query Match 19.3%; Score 200.5; DB 3; Length 154;

Best Local Similarity 29.8%; Pred. No. 1.7e-07;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDQOA 75
Db 9 HPQNNISICTCKPKGTLYNDPCPGQDTCRECEISFTASENHLR-HCLSCSKCRKEM 67
Qy 76 SQVALENCNSAVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132
Db 68 GQVEISSCTVDRDTCVCGCRKNQRYHWSNLFQC-----FNCSLCLN-GTVH----LSCQ 117
Qy 133 RRDTDCGTCPLGFVEHGDGCVSCPTSTLGSCE--RCAAVC 171
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 153

RESULT 3

ADA49698

ID ADA49698 standard; protein; 154 AA.

XX ADA49698;

XX 20-NOV-2003 (first entry)

XX Extracellular region of human TNFR1 (htNFR1) protein.

XX Apo-2 ligand inhibitor; Apo-2L; Apo-3; apoptosis; affinity;
KW competitive-type receptor; binding assay; cancer cell; human;
KW TNF receptor family; htNFR1; cytostatic.

XX Homo sapiens.

XX US2002192729-A1.

XX 19-DEC-2002.

XX PF 28-MAR-2002; 2002US-00112793.
XX PR 01-APR-1996; 96US-00625328.
XX PR 23-SEP-1996; 96US-00710802.
XX PR 31-MAR-1997; 97US-00828683.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ;
XX DR WPI; 2003-657226/62.
XX PT Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
XX PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
XX PT in diagnostic assays.
XX PS Disclosure; Fig 2; 53pp; English.
XX CC The present invention relates to the isolation of a biologically active
XX CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide
XX CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The
XX CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI
XX CC is useful for generating antibodies, as standards in assays for Apo-3 or
XX CC Apo-2LI, in affinity purification techniques, and in competitive-type
XX CC receptor binding assays when labelled with radioiodine, enzymes or
XX CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
XX CC inducing apoptosis in cancer cells, and thus have therapeutic utility.
XX CC The present sequence represents the extracellular region of a human TNF
XX CC receptor family protein. This sequence is compared with the extracellular
XX CC region of human Apo-2LI.
XX SQ Sequence 154 AA;
Query Match 19.3%; Score 200.5; DB 6; Length 154;
Best Local Similarity 29.8%; Pred. No. 1.7e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 16 HKKIGLCRCGCPAGHYLKAPCTPCGNSGTCVCPQDTFLAWENHNHSECARCOACDQA 75
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67
QY 76 SQVALENCASVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLGALHRRHRLCS 132
Db 68 QGVEISSCTVDRDTCVCGCRKNQRYHWSENLFCQ-----FNCSLCLN-GTVH----LSCQ 117
QY 133 RRDTDCGTCGFGYEHGDCVSCPTSTLGSCEP---RCAAVC 171
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153
RESULT 4
ID ADL17741 standard; protein; 154 AA.
XX AC ADL17741;
XX DT 06-MAY-2004 (first entry)
XX DE Human tumour necrosis factor receptor-I cysteine rich motif.
XX KW Human; apoptosis inducing molecule II; AIM II; antibody;
XX KW tumour necrosis ligand superfamily; lymphotoxin-beta receptor; TR6;
XX KW TRAIL receptor 6; lymphadenopathy; aberrant bone development;
XX KW autoimmune disease; graft-versus-host disease; rheumatoid arthritis;
XX KW osteoarthritis; cancer; apoptosis.
XX OS Homo sapiens.
XX PN US6635743-B1.
XX PD 21-OCT-2003.
XX XX

XX PF 10-MAR-2000; 2000US-00523323.
XX PR 22-MAR-1996; 96US-0013923P.
XX PR 31-OCT-1996; 96US-0030157P.
XX PR 21-MAR-1997; 97US-00822953.
XX PR 07-JAN-1998; 98US-00003886.
XX PR 20-FEB-1998; 98US-00027287.
XX PR 20-FEB-1998; 98US-0075409P.
XX PR 19-FEB-1999; 99US-00252656.
XX PR 11-MAR-1999; 99US-0124041P.
XX PR 06-JUN-1999; 99US-0137457P.
XX PR 06-JUL-1999; 99US-0142657P.
XX PR 11-AUG-1999; 99US-0148326P.
XX PR 02-DEC-1999; 99US-0168380P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ebner R, Yu G, Ruben SM, Ullrich S, Zhai Y;
XX DR WPI; 2003-810570/76.
XX CC New antibody that binds to human Apoptosis Inducing Molecule II (AIM II)
XX CC protein, useful for preparing a composition for treating e.g.,
XX CC lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis
XX CC or cancer.
XX CC Example 13; SEQ ID NO 53; 163pp; English.
XX PS The invention relates to an isolated antibody or its portion binding to a
XX CC protein comprising a protein whose sequence comprises an immunogenic
XX CC fragment of the amino acid residues 68-240 of the Human Apoptosis
XX CC inducing molecule II, AIM II, appearing as ADL17690 or a protein whose
XX CC sequence comprises a fragment of amino acid residues 68-240, where the
XX CC fragment comprises at least 30 or 50 amino acid residues. Also included
XX CC are a hybridoma that produces the antibody, a method of detecting in a
XX CC biological sample a protein that binds the antibody or its portion, a
XX CC composition comprising the antibody and a carrier and an isolated cell
XX CC that produces the antibody. Human AIM II is a member of the tumour
XX CC necrosis ligand superfamily and has been shown to bind lymphotoxin-beta
XX CC receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing
XX CC a composition for treating e.g., lymphadenopathy, aberrant bone
XX CC development, autoimmune disease, graft-versus-host disease, rheumatoid
XX CC arthritis, osteoarthritis or cancer (many other diseases and conditions
XX CC are listed in the specification). The present sequence represents a
XX CC cysteine-rich motif from a protein thought to bind AIM II.
XX SQ Sequence 154 AA;
Query Match 19.3%; Score 200.5; DB 7; Length 154;
Best Local Similarity 29.8%; Pred. No. 1.7e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 16 HKKIGLCRCGCPAGHYLKAPCTPCGNSGTCVCPQDTFLAWENHNHSECARCOACDQA 75
Db 9 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 67
QY 76 SQVALENCASVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLGALHRRHRLCS 132
Db 68 QGVEISSCTVDRDTCVCGCRKNQRYHWSENLFCQ-----FNCSLCLN-GTVH----LSCQ 117
QY 133 RRDTDCGTCGFGYEHGDCVSCPTSTLGSCEP---RCAAVC 171
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 153
RESULT 5
ID ADJ56814 standard; protein; 154 AA.
XX AC ADJ56814;
XX DT 06-MAY-2004 (first entry)
XX XX

DE Human TNFR-I cysteine-rich motif.

XX Apoptosis inducing molecule II; AIM II; TNF; tumour necrosis factor;

KW therapy; graft versus host disease; immunodeficiency; cancer;

KW autoimmune disease; multiple sclerosis; type I diabetes;

KW rheumatoid arthritis; primary biliary cirrhosis; aplastic anaemia;

KW myelodysplasia; systemic lupus erythematosus;

KW idiopathic thrombocytopenic purpura; cellular response;

KW T-cell activation; molecular weight marker; human; TNF receptor; TNFR.

XX Homo sapiens.

OS

XX US2004009147-A1.

XX

XX 15-JAN-2004.

XX

XX 28-FEB-2003; 2003US-00375680.

XX

XX 22-MAR-1996; 96US-0013923P.

PR 31-OCT-1996; 96US-0030157P.

PR 21-MAR-1997; 97US-00822953.

PR 07-JAN-1998; 98US-00003886.

PR 20-FEB-1998; 98US-00027287.

PR 19-FEB-1998; 98US-0075409P.

PR 11-MAR-1999; 99US-00252656.

PR 04-JUN-1999; 99US-0124041P.

PR 06-JUL-1999; 99US-012657P.

PR 11-AUG-1999; 99US-0148326P.

PR 02-DEC-1999; 99US-0168380P.

PR 10-MAR-2000; 2000US-00523323.

PR 01-MAR-2002; 2002US-0360234P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX

XX Ebner R, Yu G, Ruben SM, Zhai Y, Ullrich S;

XX WPI; 2004-201265/19.

XX

XX Isolated apoptosis inducing molecule II polypeptide, useful for treating,

PT preventing, ameliorating, diagnosing or prognosing autoimmune diseases

PT such as multiple sclerosis, rheumatoid arthritis, aplastic anemia.

XX

XX Example 13; SEQ ID NO 53; 189pp; English.

XX

XX The invention relates to apoptosis inducing molecule II (AIM II), a TNF

CC (tumour necrosis factor)-ligand superfamily member and its corresponding

CC nucleic acid sequence. The invention is useful for preventing, treating,

CC ameliorating, diagnosing or prognosing graft versus host disease,

CC immunodeficiency, cancer, autoimmune diseases such as multiple sclerosis,

CC type I diabetes, rheumatoid arthritis, primary biliary cirrhosis,

CC aplastic anaemia, myelodysplasia, systemic lupus erythematosus and

CC idiopathic thrombocytopenic purpura. It is useful for screening or

CC identifying compounds capable of enhancing or inhibiting cellular

CC response induced by AIM II, for inhibiting, blocking or reducing T-cell

CC activation. AIM II is useful as a molecular weight marker on SDS-PAGE

CC gels or on gel filtration columns. The present sequence is a cysteine-

CC rich motif of human TNF receptor (TNFR) family member.

XX

SQ Sequence 154 AA;

Query Match 19.3%; Score 200.5; DB 8; Length 154;

Best Local Similarity 29.8%; Pred. No. 1.7e-07;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQA 75

Db 9 HPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCRKEM 67

Qy 76 SQVALENCNSAVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCDLCGALHRRHRLCS 132

Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSICLN-GTVH----LSCQ 117

Qy 133 RRDTDCGTCLPGFVEHGDGCVSCPTSLGSCPE--RCAAVC 171

Db 118 EKQNTVCTCHAGFLRENEVCSC-----SNCKKSELECTKLC 153

RESULT 6

ABG74752

ID ABG74752 standard; protein; 161 AA.

XX ABG74752;

AC

XX 14-MAY-2003 (first entry)

DT

XX Human TNF binding protein fragment.

DE

XX TNF; human; tumour necrosis factor; tumour necrosis factor receptor;

KW TNF-R; tumour necrosis factor binding protein; TNF-BP; tumour.

XX Homo sapiens.

XX EP393438-A.

PN

XX 24-OCT-1990.

PD

XX 06-APR-1990; 90EP-00106624.

PF

XX 21-APR-1989; 89DE-03913101.

PR 21-JUN-1989; 89DE-03920282.

PR

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

PA (SYND) SYNERGEN INC.

PA

XX Hauptmann R, Himmeler A, Maurerfogy I, Stratowa C;

PI

XX WPI; 1990-321987/43.

DR

XX DNA encoding TNF binding protein and TNF- receptor - used in tumour

PT treatment and to understand mechanisms to TNF action.

PT

XX Claim 23; Page 34; 51pp; German.

PS

XX This invention describes novel polynucleotide sequences encoding tumour

CC necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP).

CC The products of the invention are useful in pharmaceutical compositions

CC for prophylaxis or treatment of human tumours and to understand the

CC mechanisms of TNF action. This sequence represents a fragment of the TNF-

CC BP described in the disclosure of the invention

XX

SQ Sequence 161 AA;

Query Match 19.3%; Score 200.5; DB 2; Length 161;

Best Local Similarity 29.8%; Pred. No. 1.8e-07;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQA 75

Db 11 HPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCRKEM 69

Qy 76 SQVALENCNSAVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCDLCGALHRRHRLCS 132

Db 70 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSICLN-GTVH----LSCQ 119

Qy 133 RRDTDCGTCLPGFVEHGDGCVSCPTSLGSCPE--RCAAVC 171

Db 120 EKQNTVCTCHAGFLRENEVCSC-----SNCKKSELECTKLC 155

RESULT 7

AAR27496

ID AAR27496 standard; protein; 161 AA.

XX AAR27496;

XX

DT 25-MAR-2003 (revised)
XX 09-MAR-1993 (first entry)
XX
DE Native 30 kD TNF inhibitor.
XX
KW Tumour necrosis factor; ethylene glycol; pharmacokinetic;
KW adult respiratory distress syndrome; rheumatoid arthritis; septic shock;
KW pulmonary fibrosis; spacer.
XX
OS Homo sapiens.
XX
XX WO9216221-A1.
XX
XX 01-OCT-1992.
XX
XX 13-MAR-1992; 92WO-US002122.
XX
XX 15-MAR-1991; 91US-00669862.
XX
XX 17-JAN-1992; 92US-00822236.
XX
XX (SYND) SYNERGEN INC.
XX
XX Thompson RC, Armes LG, Evans RJ, Brewer MT, Kohno T;
XX
XX WPI; 1992-348933/42.
XX
XX New ethylene! glycolated polypeptide(s) with improved pharmacokinetic
XX properties - for treating e.g. TNF and IL-1 mediated diseases, e.g. adult
XX respiratory distress syndrome, rheumatoid arthritis, septic shock etc.
XX
XX Claim 54; Fig 2; 100pp; English.
XX
XX The sequence shows a native 30 kD TNF inhibitor which may be modified to
XX contain at least one non-native cysteine residue, pref. at positions 1,
XX 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-
XX peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such
XX TNF inhibitor mols. may be linked via this non-peptidic spacer. The
XX modified polypeptides show improved pharmacokinetic properties, i.e.
XX increased mol. wt. hence reduced clearance rate following s.c. or
XX systemic administration, increased sol. of native TNF inhibitors, and
XX reduced antigenicity. The polypeptides may be used for treatment of TNF
XX mediated diseases such as adult respiratory distress syndrome, pulmonary
XX fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic
XX shock. The same method may be applied to the interleukin-1 receptor
XX antagonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct
XX CN field.)
XX
SQ Sequence 161 AA;

Query Match 19.3%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKTGLFCRCGCPAGHYLKAPCTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQA 75
Db 11 HPQNNISICTKCHGTYLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 69

Qy 76 SQVALENCASAVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCS 132
Db 70 GQVEISSCTVDRDTCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH---LSCQ 119

Qy 133 RRDTDCGTCPLGPFYEHGDCVCSTLGSQPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 155

RESULT 8
AAW59664
ID AAW59664 standard; protein; 161 AA.
XX
AC AAW59664;
XX
DT 28-SEP-1998 (first entry)

XX Human soluble tumour necrosis factor receptor type I.
XX
XX Human; tumour necrosis factor; TNF; TNF receptor type I;
KW inflammatory disease; leukaemia; TNF binding protein;
KW anti-inflammatory drug; methotrexates.
XX
OS Homo sapiens.
XX
XX WO9824463-A2.
XX
XX 11-JUN-1998.
XX
XX 08-DEC-1997; 97WO-US022733.
XX
XX 06-DEC-1996; 96US-0032587P.
XX
XX 23-JAN-1997; 97US-0036355P.
XX
XX 07-FEB-1997; 97US-0039315P.
XX
XX 09-JUL-1997; 97US-0052023P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Bendele AM, Sennello RM, Edwards CK;
XX
XX WPI; 1998-333039/29.
XX
XX N-ESDB; AAV41548.
XX
XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by
XX administering tumour necrosis factor binding protein and at least one
XX additional anti-inflammatory drug, e.g. methotrexate.
XX
XX Disclosure; Fig 1; 104pp; English.
XX
XX This is the amino acid sequence of the human tumour necrosis factor
XX receptor type I, used in the method of the invention involving the
XX treatment of acute or chronic inflammatory disease such as leukaemia by
XX administering tumour necrosis factor binding protein and at least one
XX additional anti-inflammatory drug, e.g. methotrexate
XX
SQ Sequence 161 AA;

Query Match 19.3%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKTGLFCRCGCPAGHYLKAPCTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQA 75
Db 11 HPQNNISICTKCHGTYLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 69

Qy 76 SQVALENCASAVADTRCGCKPGWFVEEC---QVSQCVSSSPFYCQPCDGCALHRRHRLCS 132
Db 70 GQVEISSCTVDRDTCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH---LSCQ 119

Qy 133 RRDTDCGTCPLGPFYEHGDCVCSTLGSQPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 155

RESULT 9
AAW52267
ID AAW52267 standard; protein; 161 AA.
XX
AC AAW52267;
XX
XX 29-JUN-1998 (first entry)
XX
XX Soluble tumour necrosis factor receptor.
XX
XX Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease;
KW tumour necrosis factor binding protein; autoimmune disease; arthritis;
KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;
KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.
XX

OS Homo sapiens.
PN WO9801555-A2.
XX
PD 15-JAN-1998.
XX
PF 09-JUL-1997; 97WO-US012244.
XX
PR 09-JUL-1996; 96US-0021443P.
PR 06-DEC-1996; 96US-0032534P.
PR 23-JAN-1997; 97US-0037737P.
PR 07-FEB-1997; 97US-0039314P.
PR 04-MAR-1997; 97US-0039792P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Fisher EF, Edwards CK, Kieft GL;
XX
XX WPI; 1998-101052/09.
DR N-PSDB; AAV19801.
XX
XX Truncated and soluble forms of tumour necrosis factor receptor - useful
PT for treating diseases involving factor, e.g. arthritis and adult
PT respiratory distress syndrome.
XX
XX Claim 1; Fig 1; 205pp; English.
PS
XX This sequence is the human soluble tumour necrosis factor receptor
CC (sTNFR). The protein was used to make the truncated sTNFR proteins of the
CC invention. The truncated sTNFR proteins and tumour necrosis factor
CC binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g.
CC arthritis, adult respiratory distress syndrome, cachexia/anorexia,
CC cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease
CC and other autoimmune diseases. Cells transformed with a vector containing
CC DNA encoding the protein may be used for production of recombinant sTNFR,
CC which may also be used for measuring the amount of sTNFR in samples and
CC to raise antibodies against sTNFR. TNBP may also be used in preparation
CC of therapeutic compositions for treating the above diseases. The sTNFR
CC proteins are well suited to large scale production (since they lack the
CC deamidation site in region 111-126, so are more stable in vivo); contain
CC fewer disulphide bonds and fewer epitopes, making them less antigenic
CC than full-length proteins
XX
SQ Sequence 161 AA;
Query Match 19.3%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 11 HPQNNISICTKCHKGTLYNDCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 69
Qy 76 SQVALENCASAVADTRCCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLCS 132
Db 70 QGVBEISCTVDRDTCVCGCRKNQRYHWSNLFCQ-----FNCSLCLN-GTVH----LSCQ 119
Qy 133 RRDTCGTCCLPGFYEHGDCVSCPTSLGSCPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155
RESULT 10
AAW89233
ID AAW89233 standard; protein; 161 AA.
XX
AC AAW89233;
XX
DT 04-MAR-1999 (first entry)
XX
DE Tumour necrosis inhibitor 30 kDa protein.
XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW

KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis.
XX
OS Homo sapiens.
XX
PN WO9849305-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US008631.
XX
PR 01-MAY-1997; 97US-00850188.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Wooden S;
XX
XX WPI; 1999-034661/03.
DR N-PSDB; AAV81732.
XX
XX New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin
PT dimerisation domain and a heterologous sequence, useful to treat TNF and
PT TNFR-mediated disorders.
XX
XX Disclosure; Fig 2; 92pp; English.
XX
XX The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are
CC used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence represents the TNF inhibitor 30 kDa protein
XX
SQ Sequence 161 AA;
Query Match 19.3%; Score 200.5; DB 2; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTPCGNGSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 11 HPQNNISICTKCHKGTLYNDCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 69
Qy 76 SQVALENCASAVADTRCCKPGWFVEC---QVSQCVSSSPFYCQCLDCGALHRRHRLCS 132
Db 70 QGVBEISCTVDRDTCVCGCRKNQRYHWSNLFCQ-----FNCSLCLN-GTVH----LSCQ 119
Qy 133 RRDTCGTCCLPGFYEHGDCVSCPTSLGSCPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLCTKLC 155
RESULT 11
AAB37676
ID AAB37676 standard; protein; 161 AA.
XX
AC AAB37676;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 30 kDa TNF inhibitor.
XX
XX TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human.

```
XX OS Homo sapiens.
XX PN US6143866-A.
XX PD 07-NOV-2000.
XX PF 19-JAN-1995; 95US-00375242.
XX PR 18-JUL-1989; 89US-00381080.
XX PR 11-DEC-1989; 89US-00450329.
XX PR 07-FEB-1990; 90US-00479661.
XX PR 19-JUL-1990; 90US-00552274.
XX PR 09-JUL-1993; 93US-00090366.
XX PA (AMGE-) AMGEN INC.
XX PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
XX PI Vanderslice RW, Vannice J, Kohno T;
XX DR WPI; 2001-006443/01.
XX DR N-PSDB; AAC83945.
XX PS Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-
XX PT native cysteine residue cross-linked with polyethylene glycol, useful for
XX PT treating inflammatory and degenerative diseases mediated by TNF.
XX PS Claim 1; Fig 19; 82pp; English.
XX CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
XX CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
XX CC agents for inhibiting the activity of TNF and interleukin (IL-1), and for
XX CC treating inflammatory and degenerative diseases mediated by TNF. The 30
XX CC kDa TNF inhibitor can inhibit TNF alpha
XX SQ Sequence 161 AA;
Query Match 19.3%; Score 200.5; DB 4; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQEA 75
Db 11 HPQNNISICTKCHKGTLYLNDPCGPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 69
Qy 76 SOVALENCASAVADTCGCKPGWFVEEC---QVSQCVSSSPFYCQPCLDGCGALHRRHRLCS 132
Db 70 GQVEISSCTVDRDTCVCGCRKNQRYHWSENUFQC-----FNCSLCLN-GTVH----LSCQ 119
Qy 133 RRDTDCGTCCLPGFYEHGDCVCSPSTLTGSCPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 155
RESULT 12
ABR62363
XX ID ABR62363 standard; protein; 161 AA.
XX AC ABR62363;
XX DT 22-SEP-2003 (first entry)
XX DE Tumour necrosis factor receptor extracellular domain.
XX KW Tumour necrosis factor; receptor; proline; protein engineering.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 23 /note= "corresponds to wild-type His34 residue"
XX FT Misc-difference 46
```

```
FT Misc-difference 76 /note= "corresponds to wild-type Ser57 residue"
FT FT /note= "corresponds to wild-type Ser87 residue"
XX PN WO2003046160-A2.
XX PD 05-JUN-2003.
XX PF 21-NOV-2002; 2002WO-EP013059.
XX PR 30-NOV-2001; 2001US-0340648P.
XX PR (ISTP ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PA Brondyk W, Jiang X, Schweickhardt RL;
XX PI WPI; 2003-523245/49.
XX PI N-PSDB; ACC84134.
XX PT Increasing expression of a protein, comprises substituting at least one
XX PT codon in the polynucleotide encoding the protein, for a codon encoding
XX PT proline.
XX PS Disclosure; Fig 4; 53pp; English.
XX CC The present sequence is the protein sequence of the extracellular domain
XX CC of the p55 tumour necrosis factor receptor (TNFR). Screening of TNFR
XX CC mutant clones using a yeast display system yielded 2 mutant clones (see
XX CC ABR62364 and ABR62365) that showed higher expression levels in yeast than
XX CC in wild-type TNFR. The first clone contained a proline residue that
XX CC substituted the native Ser-87 residue (position 76 of the present
XX CC sequence). The other clone contain a proline residue that substituted the
XX CC native His-34 residue (23 of the present sequence) and also an isoleucine
XX CC residue that substituted the native Ile-57 residue (46 of the present
XX CC sequence) of TNFR. The invention provides methods of increasing protein
XX CC expression levels by substituting an amino acid residue with proline,
XX CC where the substitution occurs within 15 (preferably within 10, and
XX CC especially within 5) amino acids of a cysteine residue. The introduction
XX CC of proline residues may assist the polypeptide to adopt a favourable
XX CC conformation that fixes the neighbouring cysteine residue into the
XX CC correct orientation for disulfide bond formation, resulting in a higher
XX CC yield of correctly folded proteins in yeast or mammalian host cells
XX SQ Sequence 161 AA;
Query Match 19.3%; Score 200.5; DB 6; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQEA 75
Db 11 HPQNNISICTKCHKGTLYLNDPCGPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 69
Qy 76 SOVALENCASAVADTCGCKPGWFVEEC---QVSQCVSSSPFYCQPCLDGCGALHRRHRLCS 132
Db 70 GQVEISSCTVDRDTCVCGCRKNQRYHWSENUFQC-----FNCSLCLN-GTVH----LSCQ 119
Qy 133 RRDTDCGTCCLPGFYEHGDCVCSPSTLTGSCPE--RCAAVC 171
Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 155
RESULT 13
ADA20577
XX ID ADA20577 standard; protein; 161 AA.
XX AC ADA20577;
XX DT 20-NOV-2003 (first entry)
XX DE Human 30kDa TNF inhibitor protein.
XX KW Human; tumour necrosis factor inhibitor; 30kDa TNF inhibitor;
```

KW 40kDa TNF inhibitor; TNF mediated pathological condition.

XX Homo sapiens.

PN US6541620-B1.

XX 01-APR-2003.

XX 07-JUN-1995; 95US-00484337.

XX 18-JUL-1989; 89US-00381080.

PR 11-DEC-1989; 89US-00450329.

PR 07-FEB-1990; 90US-00479661.

PR 19-JAN-1995; 95US-00375242.

XX (ANGE-) ANGEN INC.

PI Brewer MT, Thompson RC, Kohno T;

XX WPI; 2003-531100/50.

DR New nucleic acid comprising a sequence that encodes a polypeptide having

XX TNF inhibitory activity, useful for manufacturing a medicament for

XX treating a pathological condition mediated by TNF.

XX Example 2; Fig 19; 85pp; English.

XX The present invention relates to the isolation of novel human tumour

CC necrosis factor (TNF) inhibitor polypeptides (designated 30kDa TNF

CC inhibitor and 40kDa TNF inhibitor), and the polynucleotide sequences

CC encoding them. Also disclosed is a fragment of the 30kDa TNF inhibitor

CC polypeptide which comprises at least one non-native cysteine residue at

CC the N-terminus, C-terminus, residue 14 or preferably 105. The

CC polynucleotide sequence encoding the 30kDa TNF inhibitor is useful for

CC manufacturing a medicament for treating a pathological condition mediated

CC by TNF. The present sequence represents human 30kDa TNF inhibitor

CC protein.

XX Sequence 161 AA;

XX Query Match 19.3%; Score 200.5; DB 6; Length 161;

XX Best Local Similarity 29.8%; Pred. No. 1.8e-07;

XX Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQA 75

DB 11 HPQNNSTCCTKCHKGTLYNDCPGPGQDTCRECESGSFTASENHLR-HCLSCSKCKREM 69

QY 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132

DB 70 GQVEISSCTVDRDTRVCGCRKNQRYHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

QY 133 RRDTDCGTCLPGFVEHGDGVCVSCPTSTLGSCEP---RCAAVC 171

DB 120 EKQNTVCTCHAGFLRENECVSC-----SNCKSECTKLC 155

RESULT 14

ADA20579

ID ADA20579 standard; protein; 161 AA.

XX ADA20579;

XX 20-NOV-2003 (first entry)

XX Human 30kDa TNF inhibitor protein.

XX Human; tumour necrosis factor inhibitor; 30kDa TNF inhibitor;

XX 40kDa TNF inhibitor; TNF mediated pathological condition.

XX Homo sapiens.

XX US6541620-B1.

XX 01-APR-2003.

XX 07-JUN-1995; 95US-00484337.

XX 18-JUL-1989; 89US-00381080.

PR 11-DEC-1989; 89US-00450329.

PR 07-FEB-1990; 90US-00479661.

PR 19-JAN-1995; 95US-00375242.

XX (ANGE-) ANGEN INC.

XX Brewer MT, Thompson RC, Kohno T;

XX WPI; 2003-531100/50.

DR N-PSDB; ADA20578.

XX New nucleic acid comprising a sequence that encodes a polypeptide having

XX TNF inhibitory activity, useful for manufacturing a medicament for

XX treating a pathological condition mediated by TNF.

XX Claim 1; Fig 20; 85pp; English.

XX The present invention relates to the isolation of novel human tumour

CC necrosis factor (TNF) inhibitor polypeptides (designated 30kDa TNF

CC inhibitor and 40kDa TNF inhibitor), and the polynucleotide sequences

CC encoding them. Also disclosed is a fragment of the 30kDa TNF inhibitor

CC polypeptide which comprises at least one non-native cysteine residue at

CC the N-terminus, C-terminus, residue 14 or preferably 105. The

CC polynucleotide sequence encoding the 30kDa TNF inhibitor is useful for

CC manufacturing a medicament for treating a pathological condition mediated

CC by TNF. The present sequence represents human 30kDa TNF inhibitor

CC protein.

XX Sequence 161 AA;

XX Query Match 19.3%; Score 200.5; DB 6; Length 161;

XX Best Local Similarity 29.8%; Pred. No. 1.8e-07;

XX Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

QY 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQA 75

DB 11 HPQNNSTCCTKCHKGTLYNDCPGPGQDTCRECESGSFTASENHLR-HCLSCSKCKREM 69

QY 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDGALHRRHRLCS 132

DB 70 GQVEISSCTVDRDTRVCGCRKNQRYHWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119

QY 133 RRDTDCGTCLPGFVEHGDGVCVSCPTSTLGSCEP---RCAAVC 171

DB 120 EKQNTVCTCHAGFLRENECVSC-----SNCKSECTKLC 155

RESULT 15

ADH78698

ID ADH78698 standard; peptide; 161 AA.

XX ADH78698;

XX 15-APR-2004 (first entry)

XX Human tumour necrosis factor receptor 1 (TNF-R1) protein; SEQ ID No 106.

XX T-cell epitope; cytokine; receptor; CD4+; CD8+; immunogenicity;

XX interferon-beta; tumour necrosis factor receptor-1; erythropoietin;

XX thrombopoietin; inflammation; cancer; anaemia;

XX human tumour necrosis factor receptor 1; TNF-R1.

XX Homo sapiens.

XX WO2003104263-A2.

XX 18-DEC-2003.

XX 26-FEB-2003; 2003WO-US005917.
XX 01-MAY-2002; 2002US-0376743P.
XX (GEMV) GENENCOR INT INC.
XX Harding FA, Power SD;
XX WPI; 2004-062306/06.
XX
XX Determining T-cell epitope of a protein (e.g. cytokine or cytokine
XX receptor); useful for reducing protein allergenicity, comprises combining
XX differentiated dendritic cells and naive T-cells with a peptide having
XX the T-cell epitope.
XX
XX Claim 4; SEQ ID NO 106; 51pp; English.
XX
XX The invention relates to a novel method for determining a T-cell epitope
XX of a protein, where the protein is selected from cytokines and cytokine
XX receptors. The method comprises combining a solution of differentiated
XX dendritic cells and naive CD4+ and/or CD8+ T-cells with a pepset of
XX peptides comprising the T-cell epitope. The composition and methods are
XX useful in reducing the immunogenicity of cytokines and cytokine receptors
XX such as interferon-beta, soluble tumour necrosis factor receptor-1,
XX erythropoietin or thrombopoietin. These modified cytokines and cytokine
XX receptors may be used for treating various conditions such as
XX inflammation, cancer or anaemia. This sequence represents the human
XX tumour necrosis factor receptor 1 (TNF-R1) protein of the invention.
XX
XX Sequence 161 AA;
XX
XX Query Match 19.3%; Score 200.5; DB 8; Length 161;
XX Best Local Similarity 29.8%; Pred. No. 1.8e-07;
XX Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
XX
XX Qy 16 HKKIGLPCRCPCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWHHNSECARCQACDEQA 75
XX Db 11 HPQNNSTCTKCHKGTLYNDPCPGQPTDCRECESGFTASENHLR-HCLSCSKCRKEM 69
XX
XX Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQCLDCGALHRRHRLCS 132
XX Db 70 QGVEISSCTVDRDTCGCRKNQYRHYSENLFQC-----FNCSICLN-GTVH----LSCQ 119
XX
XX Qy 133 RRDTCGTCPLPGFYEHGDCGVSCPTSTILGSCPE--RCAAVC 171
XX Db 120 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 155

Search completed: June 27, 2005, 14:18:38
Job time : 163 secs

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no.	score	match	length	id	description
1	210.5	20.3	162	9	US-09-798-789-12
2	210.5	20.3	162	14	US-10-218-102-422
3	205.5	19.8	162	9	US-09-798-789-13
4	205.5	19.8	162	9	US-09-798-789-20
5	205.5	19.8	162	14	US-10-218-102-423
6	205.5	19.8	162	14	US-10-218-102-430
7	203.5	19.6	162	9	US-09-798-789-11
8	203.5	19.6	162	14	US-10-218-102-421
9	203	19.6	173	9	US-09-899-429A-16
10	201.5	19.4	162	9	US-09-798-789-19
11	201.5	19.4	162	9	US-09-798-789-21
					Sequence 12, Appl
					Sequence 422, Appl
					Sequence 13, Appl
					Sequence 20, Appl
					Sequence 423, Appl
					Sequence 430, Appl
					Sequence 11, Appl
					Sequence 421, Appl
					Sequence 16, Appl
					Sequence 19, Appl
					Sequence 21, Appl

76 SOVALENCSAVANTBCCGCKPGWEVECOVSOVSSSPFVCOBCT.NC--GAI.HR

76 SOVALENCSAVADTRCGCKPGWFVECVSQVSSSPFYCQPCLCD--GALHRHTRLCLSR 133

Db 71 GQVEISSCTVDRDTCVCGCRKN-----QVRHYETENEFFCNCSLCLNGTVH-----LSCQE 121
Qy 134 RDTDCGTCLPGFYHGHGCVSCPTSTLGSQPE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 2

US-10-218-102-422
; Sequence 422, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 422
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-422

Query Match 20.3%; Score 210.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 2.6e-09;
Matches 48; Conservative 20; Mismatches 73; Indels 19; Gaps 6;

Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA 75
Db 12 HPQNNISCTCTKCHKGTLYNDPCPGQDTCRECESGSFTASE-EHKRECLRCRCRDKM 70
Qy 76 SOVALENCSAVADTRCGCKPGWFVECOVSQCVSSSPFYCOPCLDC--GALHRHTRLLCSR 133
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QVRHYETENEFFCNCSLCLNGTVH-----LSCQE 121
Qy 134 RDTDCGTCLPGFYHGHGCVSCPTSTLGSQPE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 3

US-09-798-789-13
; Sequence 13, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427

; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-13

Query Match 19.8%; Score 205.5; DB 9; Length 162;
Best Local Similarity 30.0%; Pred. No. 6.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA 75
Db 12 HPQNNISCTCTKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-DCIQCSCQKKHD 70
Qy 76 SOVALENCSAVADTRCGCKPGWFVECOVSQCVSSSPFYCOPCLDC--GALHRHTRLLCSR 133
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QVRHYDHENRFYCNCSLCLNGTVH-----LSCQE 121
Qy 134 RDTDCGTCLPGFYHGHGCVSCPTSTLGSQPE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 4

US-09-798-789-20
; Sequence 20, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-20

Query Match 19.8%; Score 205.5; DB 9; Length 162;
Best Local Similarity 30.4%; Pred. No. 6.5e-09;
Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;

Qy 16 HKKIGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA 75
Db 12 HPQNNISCTCTKCHKGTLYNDPCPGQDTCRECESGSFTASENHLR-HCLSCSKCRKEM 70
Qy 76 SOVALENCSAVADTRCGCKPGWFVECO---VSQCVSSSPFYCOPCLDCGALHRHTRLLCS 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQYHYQSENLFCQ-----FNCSICLN-GTVH-----LSCQ 120
Qy 133 RRTDCTCLPGFYHGHGCVSCPTSTLGSQPE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 5

US-10-218-102-423
; Sequence 423, Application US/10218102

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; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 423
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-423

Query Match          19.8%; Score 205.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 6.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARQACDQEA 75
Db 12 HPQNNISCTCKCHKGTLYLNDPCPGQDTCRECSGFTASENHLR-DCILQCSQCKKHD 70

Qy 76 SOVALENCASAVADTRCGCKPGWFVEVCQVSSSPFYCQPCLDGALHRRHRLCSR 133
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QYRHYDHENRFYCFNCSLCLNGTVH----LSCQE 121

Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

; RESULT 6
US-10-218-102-430
; Sequence 430, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 430
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-430

Query Match          19.8%; Score 205.5; DB 14; Length 162;
Best Local Similarity 30.4%; Pred. No. 6.5e-09;
Matches 49; Conservative 20; Mismatches 71; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARQACDQEA 75
Db 12 HPQNNISCTCKCHKGTLYLNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCKEM 70

Qy 76 SOVALENCASAVADTRCGCKPGWFVEVCQVSSSPFYCQPCLDGALHRRHRLCSR 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQYRHYQSENLFCQ-----FNCSLCLN-GTVH----LSCQ 120

Qy 133 RRTDTCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

; RESULT 7
US-09-798-789-11
; Sequence 11, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 11
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-11

Query Match          19.6%; Score 203.5; DB 9; Length 162;
Best Local Similarity 30.0%; Pred. No. 9.3e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTPCGNSTCLVCPQDTFLAWENHNHSECARQACDQEA 75
Db 12 HPQNNISCTCKCHKGTLYLNDPCPGQDTCRECSGFTASENHLRT-CLSCSKCKEM 70

Qy 76 SOVALENCASAVADTRCGCKPGWFVEVCQVSSSPFYCQPCLDGALHRRHRLCSR 133
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QYRHYVASENKFQCFNCSLCLNGTVH----LSCQE 121

Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

; RESULT 8
US-10-218-102-421
; Sequence 421, Application US/10218102
; Publication No. US20030130827A1
; GENERAL INFORMATION:
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```
; APPLICANT: Bentzien, Joerg
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hayes, Robert J.
; APPLICANT: Vielmetter, Jost
; TITLE OF INVENTION: Protein Design Automation for Protein Libraries
; FILE REFERENCE: A-67229-11/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/218,102
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US 09/927,790
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,545
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/324,899
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/351,937
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/352,103
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 421
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-218-102-421

Query Match      19.6%; Score 203.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 9.3e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19; Gaps 6;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQA 75
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHRLT-CLSCSKCLKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVECVSQCVSSSPFYCQPCLDG--GALHRHRLTLCRSR 133
Db 71 GQVEISSCTVDRDTCVCGCRKN-----QYRHYASENKQCFNCSLCLNGTVH----LSCQE 121

Qy 134 RDTDCGTCLPGFYEHGDCVSCPTSTLGSCEP--RCAAVC 171
Db 122 KQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 9
US-09-899-429A-16
; Sequence 16, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hammler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-Bp sequence
US-09-899-429A-16

Query Match      19.6%; Score 203; DB 9; Length 173;
Best Local Similarity 29.4%; Pred. No. 1.1e-08;
Matches 52; Conservative 20; Mismatches 81; Indels 24; Gaps 8;

Qy 3 GTRSPP---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN 59
Db 7 GDREKRDVCPQGGKYIHPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASEN 66

Qy 60 HHNSECARCOACDEQASQVALENCASAVADTRCGCKPGWFVECVSQCVSSSPFYCQPC 116
Db 67 HLR-HCLSCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYASENLFQC-----FNCSL 120

Qy 117 CLDCGALHRHRLTLCRRDTCGTCPLGFGYEHGDCVSCPTSTLGSCEP--RCAAVC 171
Db 121 CLN-GTVH----LSCQEKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 167

RESULT 10
US-09-798-789-19
; Sequence 19, Application US/09798789
; Patent No. US20020009780A1
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil
; APPLICANT: Filikov, Anton
; TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
; TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: A-68990-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/798,789
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/186,427
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-19

Query Match      19.4%; Score 201.5; DB 9; Length 162;
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 21; Mismatches 71; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQA 75
Db 12 HPQNNISCTCKCHKGTLYNDPCPGQDTCRECSGSFTASENHRL-HCLSCSKCRKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVECVSQCVSSSPFYCQPCLDGALHRHRLTLCRS 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQYRHYASENLFQC-----FNCSICLN-GTVH----LSCQ 120

Qy 133 RDTDCGTCLPGFYEHGDCVSCPTSTLGSCEP--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 11
US-09-798-789-21
; Sequence 21, Application US/09798789
; Patent No. US20020009780A1
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GENERAL INFORMATION:
APPLICANT: Dahiyat, Bassil
APPLICANT: Filikov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: A-68990-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/798,789
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 21
LENGTH: 162
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-21

Query Match 19.4%; Score 201.5; DB 9; Length 162;
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 75
Db 12 HPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLR-HCLGCSKCQKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVEQ----QVSQCVSSSPFYCQPCDCLGALHRRHRLCS 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQRYHNSENLFCQ-----FNCSLCLN-GTVH----LSCQ 120

Qy 133 RRDTDGCTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 13
US-10-218-102-431
Sequence 431, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Desjarlais, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: US 09/927,790
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/311,545
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 60/324,899
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/351,937
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/352,103
NUMBER OF SEQ ID NOS: 432
SOFTWARE: PatentIn version 3.1
SEQ ID NO 431
LENGTH: 162
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-218-102-431

Query Match 19.4%; Score 201.5; DB 14; Length 162;
Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQA 75
Db 12 HPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLR-HCLGCSKCQKEM 70

Qy 76 SQVALENCASAVADTRCGCKPGWFVEQ----QVSQCVSSSPFYCQPCDCLGALHRRHRLCS 132
Db 71 GQVEISSCTVDRDTCVCGCRKNQRYHNSENLFCQ-----FNCSLCLN-GTVH----LSCQ 120

Qy 133 RRDTDGCTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 121 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSLECTKLC 156

RESULT 14
US-09-800-909-3
Sequence 3, Application US/09800909
Patent No. US2001001983A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David

Query Match 19.4%; Score 201.5; DB 14; Length 162;

APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,909
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,862
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-800-909-3

Query Match 19.3%; Score 200.5; DB 9; Length 153;
Best Local Similarity 29.8%; Pred. No. 1.5e-08;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPGCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 9 HPQNNISICTKCHKGTLYNDCPGPGQDTCRECESGSFTASENHLR-HCLSCSKCRKEM 67
Qy 76 SQVALENCNSAVADTRCGCKPGWFVEC---QVSQCVSPPFYCQPCDLCGALHRRHRLICS 132
Db 68 GQVEISSCTVDRDRTVCGCRKNQRYHWSNLFQC-----FNCSLCN-GTVH----LSCQ 117
Qy 133 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 171
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSECTKLC 153

RESULT 15
US-09-884-987-4
; Sequence 4, Application US/09884987
; Patent No. US2020102653A1
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu et al

TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REFERENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 153
TYPE: PRT
ORGANISM: Homo sapiens
US-09-884-987-4
Query Match 19.3%; Score 200.5; DB 9; Length 153;
Best Local Similarity 29.8%; Pred. No. 1.5e-08;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPGCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQA 75
Db 9 HPQNNISICTKCHKGTLYNDCPGPGQDTCRECESGSFTASENHLR-HCLSCSKCRKEM 67
Qy 76 SQVALENCNSAVADTRCGCKPGWFVEC---QVSQCVSPPFYCQPCDLCGALHRRHRLICS 132
Db 68 GQVEISSCTVDRDRTVCGCRKNQRYHWSNLFQC-----FNCSLCN-GTVH----LSCQ 117
Qy 133 RRDTDCGTCLPGFVEHGDGCVSCPTSTLGSCE--RCAAVC 171
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKKSECTKLC 153

Search completed: June 27, 2005, 14:35:11
Job time : 160 secs

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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:15:57 ; Search time 42 Seconds
(without alignments)
309.260 Million cell updates/sec

Title: US-10-081-280-6_COPY_25_198

Perfect score: 1038
Sequence: 1 QGTRSPRCAGDFHKKIG.....CPTSTLGSCEPCCAACGWR 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 380303

Minimum DB seq length: 0
Maximum DB seq length: 174

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200.5	19.3	153	2	US-08-219-237B-4
2	200.5	19.3	153	3	US-08-477-347-12
3	200.5	19.3	153	3	US-08-476-862-3
4	200.5	19.3	153	3	US-08-468-560C-4
5	200.5	19.3	153	4	US-09-800-909-3
6	200.5	19.3	153	4	US-09-800-908-12
7	200.5	19.3	154	4	US-08-828-683A-12
8	200.5	19.3	154	4	US-09-523-323-53
9	200.5	19.3	161	3	US-09-326-394-2
10	198.5	19.1	154	2	US-08-232-087A-10
11	196	18.9	139	3	US-08-706-945D-129
12	185	17.8	123	3	US-09-855-266A-13
13	182	17.5	155	3	US-09-146-950-4
14	182	17.5	159	3	US-09-146-950-20
15	181.5	17.5	161	4	US-08-523-323-56
16	170.5	16.4	158	1	US-08-050-319B-54
17	170.5	16.4	158	2	US-08-465-982-54
18	164.5	15.8	148	3	US-09-411-722-2
19	164.5	15.8	148	4	US-09-855-266A-2
20	162.5	15.7	119	2	US-08-219-237B-3
21	162.5	15.7	119	3	US-08-477-347-14
22	162.5	15.7	119	3	US-08-476-862-5
23	162.5	15.7	119	3	US-08-468-560C-3
24	162.5	15.7	119	4	US-08-828-683A-15
25	162.5	15.7	119	4	US-09-800-909-5
26	162.5	15.7	119	4	US-09-800-908-14
27	162.5	15.7	128	3	US-09-180-100-9

28	162.5	15.7	143	3	US-09-180-100-10	Sequence 10, Appl
29	162.5	15.7	144	3	US-09-180-100-21	Sequence 21, Appl
30	162.5	15.7	157	3	US-09-180-100-15	Sequence 15, Appl
31	162.5	15.7	159	3	US-09-180-100-23	Sequence 23, Appl
32	162.5	15.7	167	4	US-08-828-683A-22	Sequence 22, Appl
33	161	15.5	167	1	US-08-050-319B-2	Sequence 2, Appl
34	161	15.5	167	1	US-08-050-319B-57	Sequence 57, Appl
35	161	15.5	167	2	US-08-465-982-2	Sequence 2, Appl
36	161	15.5	167	2	US-08-465-982-57	Sequence 57, Appl
37	158.5	15.3	124	1	US-08-050-319B-4	Sequence 4, Appl
38	158.5	15.3	124	2	US-08-465-982-4	Sequence 4, Appl
39	155.5	15.0	133	4	US-09-612-033B-6	Sequence 6, Appl
40	152.5	14.7	157	1	US-08-050-319B-50	Sequence 50, Appl
41	152.5	14.7	157	2	US-08-465-982-50	Sequence 50, Appl
42	141.5	13.6	170	4	US-09-523-323-57	Sequence 57, Appl
43	140.5	13.5	170	4	US-08-828-683A-14	Sequence 14, Appl
44	136	13.1	162	2	US-08-219-237B-7	Sequence 7, Appl
45	136	13.1	162	3	US-08-477-347-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-219-237B-4
; Sequence 4, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; City: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-4

Query Match 19.3% Score 200.5; DB 2; Length 153;
Best Local Similarity 23.8%; Pred. No. 7.7e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Oy 16 HKKTGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWHNHNSCARCOACDQQA 75
Db 9 HPQNNISCTCKHKGTYLYNDCPGQDTCRECSGFTASENHLR-HCLSCSKCKREM 67

Db 118 EKQNTVCTCHAGFFLURENECVSC-----SNCKKSLECTKLC 153

RESULT 4

US-08-468-560C-4

; Sequence 4, Application US/08468560C

; Patent No. 6270998

; GENERAL INFORMATION:

; APPLICANT: NAGATA, Shigekazu

; APPLICANT: ITOH, Naoto

; APPLICANT: YONEHARA, Shin

; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE

; TITLE OF INVENTION: ANTIGEN

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.

; STREET: P.O. BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,560C

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURPHY JR., GERLAD M.

; REGISTRATION NUMBER: 28,977

; REFERENCE/DOCKET NUMBER: 20-4393P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-205-8000

; TELEFAX: 703-205-8050

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 153 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-468-560C-4

Query Match 19.3%; Score 200.5; DB 3; Length 153;

Best Local Similarity 29.8%; Pred. No. 7.7e-11;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDQQA 75

Db 9 HPQNNISCTCKHGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67

Qy 76 SQVALENSAVADTRCGCKPGWFVEEC-----QVSQCVSPPFYCQPCDCLDGAHRRHRLCLS 132

Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSCLN-GTVH-----LSCQ 117

Qy 133 RRDTDCGTCGCLPGFVHGDCVCSCPTSLGSCPE--RCAAVC 171

Db 118 EKQNTVCTCHAGFFLURENECVSC-----SNCKKSLECTKLC 153

RESULT 5

US-09-800-909-3

; Sequence 3, Application US/09800909

; Patent No. 655111

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BIGDA, Jacek

; APPLICANT: BELETSKY, Igor

; APPLICANT: METT, Igor

; APPLICANT: ENGELMANN, Hartmut

; TITLE OF INVENTION: TNF INHIBITORS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/800,909

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/476,862

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 94039

; FILING DATE: 06-APR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 91229

; FILING DATE: 06-AUG-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 90339

; FILING DATE: 18-MAY-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH=12A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 153 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-800-909-3

Query Match 19.3%; Score 200.5; DB 4; Length 153;

Best Local Similarity 29.8%; Pred. No. 7.7e-11;

Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDQQA 75

Db 9 HPQNNISCTCKHGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 67

Qy 76 SQVALENSAVADTRCGCKPGWFVEEC-----QVSQCVSPPFYCQPCDCLDGAHRRHRLCLS 132

Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHWSENLFQC-----FNCSCLN-GTVH-----LSCQ 117

Qy 133 RRDTDCGTCGCLPGFVHGDCVCSCPTSLGSCPE--RCAAVC 171

Db 118 EKQNTVCTCHAGFFLURENECVSC-----SNCKKSLECTKLC 153

RESULT 6

US-09-800-908-12

; Sequence 12, Application US/09800908

; Patent No. 6602993

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BIGDA, Jacek

; APPLICANT: BELETSKY, Igor

; APPLICANT: METT, Igor

; TITLE OF INVENTION: TNF LIGANDS

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,908
FILING DATE: 08-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,347
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
STRANDEDNESS: single
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-800-908-12
Query Match 19.3%; Score 200.5; DB 4; Length 153;
Best Local Similarity 29.8%; Pred. No. 7.7e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQA 75
Db 9 HPQNNISCTCKCHKGTLYNDCPGPGQDTCRECSGSFTASENHRL-HCLSCSKCKREM 67
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQPCLDGALHRRHRLCLS 132
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQC-----FNCSLCIN-GTVH----LSCQ 117
Qy 133 RRDTCGTCCLPGFVHGDCGVCSTPTSLGSCPE--RCAAVC 171
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153
RESULT 7
US-08-828-683A-12
Sequence 12, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-828-683A-12
Query Match 19.3%; Score 200.5; DB 4; Length 154;
Best Local Similarity 29.8%; Pred. No. 7.7e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQA 75
Db 9 HPQNNISCTCKCHKGTLYNDCPGPGQDTCRECSGSFTASENHRL-HCLSCSKCKREM 67
Qy 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSCVSSSPFYCQPCLDGALHRRHRLCLS 132
Db 68 GQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQC-----FNCSLCIN-GTVH----LSCQ 117
Qy 133 RRDTCGTCCLPGFVHGDCGVCSTPTSLGSCPE--RCAAVC 171
Db 118 EKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKLC 153
RESULT 8
US-09-523-323-53
Sequence 53, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000C
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/142,657
EARLIER FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 60/124,041
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 09/252,656
EARLIER FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 60/075,409
EARLIER FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 60/013,923
EARLIER FILING DATE: 1996-03-22
EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
US-09-523-323-53

Query Match 19.3%; Score 200.5; DB 4; Length 154;
Best Local Similarity 29.8%; Pred. No. 7.7e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 16 HKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQQA 75
DB 9 HPQNSICTCKHGTLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCRKEM 67
QY 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLGALHHRHRLICS 132
DB 68 GQVEISSCTVDRTVCGCRKNQRYHWSNLFCQ-----FNCSLCLN-GTVH---LSCQ 117
QY 133 RRDTCGTCLPGFVGHGDCVSCPTSLGSCPE--RCAAVC 171
DB 118 EKQNTVCTCHAGFLRENECVSC-----SNCKKSLECTKLC 153

RESULT 9
US-09-326-394-2
Sequence 2, Application US/09326394
Patent No. 6306820
GENERAL INFORMATION:
APPLICANT: Bendele, Alison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Edwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,394
FILING DATE: 08-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,587
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,355
FILING DATE: 23-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,315
FILING DATE: 07-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/052,023

FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zindrick, Thomas K.
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: A-430D
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-326-394-2

Query Match 19.3%; Score 200.5; DB 3; Length 161;
Best Local Similarity 29.8%; Pred. No. 8.1e-11;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 16 HKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQQA 75
DB 11 HPQNSICTCKHGTLYNDPCPGQDTCRECSGFTASENHLR-HCLSCSKCRKEM 69
QY 76 SQVALENCASAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCDCLGALHHRHRLICS 132
DB 70 GQVEISSCTVDRTVCGCRKNQRYHWSNLFCQ-----FNCSLCLN-GTVH---LSCQ 119
QY 133 RRDTCGTCLPGFVGHGDCVSCPTSLGSCPE--RCAAVC 171
DB 120 EKQNTVCTCHAGFLRENECVSC-----SNCKKSLECTKLC 155

RESULT 10
US-08-232-087A-10
Sequence 10, Application US/08232087A
Patent No. 5866372
GENERAL INFORMATION:
APPLICANT: Stein, Harald
APPLICANT: D rkoop, Horst
APPLICANT: Latza, Ute
TITLE OF INVENTION: Lymphoid CD30-Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,087A
FILING DATE: 08-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 756-103P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal

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;
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..154
; OTHER INFORMATION: /note= "TNPR1, see Fig. 5"
US-08-232-087A-10

Query Match      19.1%; Score 198.5; DB 2; Length 154;
Best Local Similarity 30.4%; Pred. No. 1.2e-10;
Matches 49; Conservative 23; Mismatches 68; Indels 21; Gaps 8;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQA 75
Db 9 HPQNNISCTTKCHKGTLYNDPCPGQDTCDECSQSFTASENHLR-HCLSCSKCKREM 67
Qy 76 SQVALENCASAVADTRCGCKPGWFVEVC---QVSQCVSSSPFYCPCLDCGALHRRHRLCS 132
Db 68 GQVEISSCTVDRDTRVCGCRKNQRYHWSENLFCQ-----FNCSICLN-GTVHLSGQ---E 118
Qy 133 RRDDTCGTCLPGFYEHGDCVSCPTSTLGSCE--RCAAVC 171
Db 119 KQNTVC-TCHAGFFLRENECVSC-----GNCKSLECTKLC 153

RESULT 11
US-08-706-945D-129
; Sequence 129, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-129

Query Match      18.9%; Score 196; DB 3; Length 139;
Best Local Similarity 31.5%; Pred. No. 1.8e-10;
Matches 45; Conservative 17; Mismatches 67; Indels 14; Gaps 5;

Qy 16 HKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQA 75
Db 8 HPQNNISCTTKCHKGTLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKREM 66
Qy 76 SQVALENCASAVADTRCGCKPGWFVEVC---QVSQCVSSSPFYCPCLDCGALHRRHRLCS 132
Db 67 GQVEISSCTVDRDTRVCGCRKNQRYHWSENLFCQ-----FNCSICLN-GTVH----LSCQ 116
Qy 133 RRDDTCGTCLPGFYEHGDCVSC 155
Db 117 EKQNTVCTCHAGFFLRENECVSC 139

RESULT 12
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 08501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
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; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-13

Query Match      17.8%; Score 185; DB 4; Length 123;
Best Local Similarity 28.8%; Pred. No. 1.5e-09;
Matches 47; Conservative 16; Mismatches 58; Indels 42; Gaps 6;

Qy 11 CAGD--FHKKIGLFCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARC 68
Db 1 CPGKYVHSKNNISICCTKCHKGTLYVSDCSPGRDTCRECEKGTFTASQNYLR-QCLSC 59
Qy 69 QACDEQAQVALENCASAVADTRCGCKPGWFVEVCQVSQVSSPFYCPCLDCGALHRRHR 128
Db 60 KTCRKEMSQVEISPCQADKDTVCCK-----ENQFQYVLSETHFCQ----- 100
Qy 129 LLCRRDTCGTCLPGFYEHGDCVSCPTSTLGSCEPCCAACV 171
Db 101 -----VDCSPCF-----NGTVTIP-----CKETONTVC 123

RESULT 13
US-09-146-950-4
; Sequence 4, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-4

Query Match      17.5%; Score 182; DB 3; Length 155;
Best Local Similarity 30.7%; Pred. No. 3.6e-09;
Matches 46; Conservative 14; Mismatches 66; Indels 24; Gaps 6;

Qy 19 IGLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNH--SECARCOACDEQAS 76
Db 11 VGSECCPKCSFGYRVKEACGELTG-TVCEPCPGTYIA---HLNGLSKLCCQCMCDPAMG 66
Qy 77 QVALENCASAVADTRCGCKPGWFVEVCQVSQVSSPFYCPCLDCGALHRRHRL---CSR 133
Db 67 LRASRNCSTENAVCGCGPGHF-----CIVQGDHCAACRAYATSSPGQRVQKGGTES 119
Qy 134 RDTCGTCLPGFYEHGDCVSCPTSTLGS 163
Db 120 QDTLCQNCPPGTFS-----PNTLLEC 141

RESULT 14
US-09-146-950-20
; Sequence 20, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
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RESULT 15
US-09-523-323-56
; Sequence 56, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323
; CURRENT FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/168,380
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 60/148,326
; EARLIER FILING DATE: 1993-08-11
; EARLIER APPLICATION NUMBER: 60/142,657
; EARLIER FILING DATE: 1993-07-06
; EARLIER APPLICATION NUMBER: 60/137,457
; EARLIER FILING DATE: 1993-06-04
; EARLIER APPLICATION NUMBER: 60/124,041
; EARLIER FILING DATE: 1993-03-11
; EARLIER APPLICATION NUMBER: 09/252,656
; EARLIER FILING DATE: 1993-02-19
; EARLIER APPLICATION NUMBER: 60/075,409
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/027,287
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: 60/013,923
; EARLIER FILING DATE: 1996-03-22
; EARLIER APPLICATION NUMBER: 60/030,157
; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 161

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	52.5	12.7	74	2	F71080	hypothetical prote	
2	50.5	12.2	71	2	G69463	conserved hypothet	
3	50.5	12.2	72	2	E63386	hypothetical prote	
4	50.5	12.2	73	2	D69499	conserved hypothet	
5	50.5	12.2	79	2	A84092	hypothetical prote	
6	49.5	12.0	78	2	H84353	hypothetical prote	
7	48	11.6	72	2	A82881	conserved hypothet	
8	47	11.4	60	2	D83610	hypothetical prote	
9	47	11.4	61	2	C63933	hypothetical prote	
10	47	11.4	67	2	A96702	unknown protein, 7	
11	46.5	11.3	64	2	G83940	hypothetical prote	
12	46.5	11.3	68	2	JH0129	repressor protein	
13	46.5	11.3	79	2	A06019	probable damage-in	
14	46	11.1	72	2	A75099	hypothetical prote	
15	46	11.1	76	2	H70576	hypothetical prote	
16	45.5	11.0	52	2	F83985	hypothetical prote	
17	45	10.9	67	2	AC1037	probable phage tai	
18	45	10.9	71	1	H70799	integrase-related	
19	45	10.9	80	2	F72303	glutaredoxin - The	
20	44.5	10.8	72	2	G91153	host factor for ly	
21	44.5	10.8	72	2	C85999	host factor for ly	
22	44.5	10.8	72	2	A49888	slx protein - Esc	
23	44.5	10.8	74	2	B75199	hypothetical prote	
24	44	10.7	67	2	AG0927	probable phage tai	
25	44	10.7	68	2	B55682	keratin 15, type I	
26	44	10.7	70	2	F81899	hypothetical prote	
27	43.5	10.5	62	2	F98971	hypothetical prote	
28	43.5	10.5	75	2	A26559	conserved hypothet	
29	43.5	10.5	75	2	C97441	hypothetical prote	

A;Accession: JH0129
A;Molecule type: DNA
A;Residues: 1-68 <SCH1>
A;Cross-references: UNIPROT:Q52350; GB:M28829; NID:g152577; PIDN:AAA26449.1; PID:g152585
A;Accession: PS0292
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-18 <SCH2>
C;Comment: This protein binds to the operator region of a promoter located at upstream of
C;Genetics:
A;Gene: cac
A;Genome: plasmid

Query Match 11.3%; Score 46.5; DB 2; Length 68;
Best Local Similarity 20.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 11; Mismatches 15; Indels 31; Gaps 2;

Qy 3 DAVPARRKKEFVRLTGLREAEIEAVEVEIGRFRDQOYEMLKRWQQPAGLGAVYAALER 62
Db 17 DAVRQARYAERMKAKGMQRKF-----WLTDDEVEALRE----- 50

Qy 63 MGLDGCVEDLRS 74
Db 51 -----CLEELKA 57

RESULT 13
AH0619
probable damage-inducible protein STY1032 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0619
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
Th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05426.1; PID:g16502187; GSPDB:GN00176
C;Genetics:
A;Gene: STY1032

Query Match 11.3%; Score 46.5; DB 2; Length 79;
Best Local Similarity 32.8%; Pred. No. 3.9e+02;
Matches 22; Conservative 8; Mismatches 24; Indels 13; Gaps 3;

Qy 15 RTGLGREAEIEAVEVEIGRFRDQOYE----MLKRWQQPAGLGAVYAALERWGLDGCVE 70
Db 9 RTKQLPEGAVPALEKELITRLQNYENCLTIRRGSD---GLSIVGAA-----DGDKK 59

Qy 71 DLRSRLQ 77
Db 60 RIQSIQ 66

RESULT 14
A75099
hypothetical protein PAB3293 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75099
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75099
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-72 <KAW>
A;Cross-references: UNIPROT:Q9UZG5; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50094
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB3293

Query Match 11.1%; Score 46; DB 2; Length 72;
Best Local Similarity 38.7%; Pred. No. 4e+02;
Matches 12; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

Qy 14 VRTGLGREAEIEAVEV--EIGRFRDQOYEML 42
Db 1 MRKGLGLNDRLQKAVLYVREKGRISKEYQGL 31

RESULT 15
H70576
hypothetical protein RV2132 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70576
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-76 <COL>
A;Cross-references: UNIPROT:O06243; GB:Z95388; GB:AL123456; NID:g3261759; PIDN:CAB08638.1
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV2132

Query Match 11.1%; Score 46; DB 2; Length 76;
Best Local Similarity 30.2%; Pred. No. 4.3e+02;
Matches 19; Conservative 8; Mismatches 14; Indels 22; Gaps 4;

Qy 15 RTGLGREAEIEAVEVEI-----GRFRDQOYEMLKRWQQPAGLGAVYA----ALBRMG 64
Db 22 RSIGLSEAVNELIRAGLTKEQVANRFQQQTYDM-----GEGIDYSNIGDAIET-- 69

Qy 65 LDG 67
Db 70 LDG 72

Search completed: June 27, 2005, 14:41:37
Job time : 40 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	59	14.3	79	55	Q93R97	pseudomonas
2	57	13.8	75	2	Q6TG30	azomonas ma
3	54.5	13.2	59	2	Q7P3Z1	fusobacteri
4	54	13.1	69	2	Q9ZXL9	bacterioph
5	54	13.1	78	2	Q6CZU0	erwinia car
6	53.5	13.0	79	2	Q87YA5	methanopyru
7	53	12.8	62	2	Q72GH9	thermus the
8	53	12.8	75	2	Q8U397	pyrococcus
9	53	12.8	78	2	Q7U9X2	synecococc
10	52.5	12.7	70	2	Q8H4R5	oryza sativ
11	52.5	12.7	74	2	Q7J992	pyrococcus
12	52.5	12.7	77	2	Q6PX4Y	staphylococ
13	52	12.6	70	2	Q93NF5	athrobacte
14	51	12.3	66	2	Q88AU2	pseudomonas
15	50.5	12.2	63	2	Q7EYN4	oryza sativ
16	50.5	12.2	70	2	Q7V7D7	prochlorococ
17	50.5	12.2	71	1	YH12_ARCFU	archaeoglob
18	50.5	12.2	72	1	YA94_ARCFU	archaeoglob
19	50.5	12.2	73	1	YJ97_ARCFU	archaeoglob
20	50.5	12.2	79	2	Q9K7J6	bacillus ha
21	50	12.1	61	2	Q8DD62	vibrio vuln
22	50	12.1	63	2	Q9MX53	ginglymosto
23	50	12.1	66	2	Q8ECW2	shewanella
24	50	12.1	72	2	Q87PB4	vibrio para
25	49.5	12.0	78	2	Q9HNM4	halobacteri
26	49	11.9	54	2	Q6K5Y5	oryza sativ
27	49	11.9	72	2	Q7MKX6	vibrio vuln
28	49	11.9	72	2	Q8D9G2	vibrio vuln
29	48.5	11.7	51	2	Q8CA05	mus musculu
30	48.5	11.7	60	2	Q883A4	pseudomonas
31	48.5	11.7	71	2	Q716N0	mycobacteri

05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 Stationary phase sigma factor (Fragment).
 Name=tpoS;
 Azomonas macrocytogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azomonas.
 NCBI_TaxID=69962;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12334;
 RA Scott A., Meakins D., Page W.J.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Sigma factors are initiation factors that promote the
 attachment of RNA polymerase to specific initiation sites and are
 then released (by similarity).
 CC -!- SIMILARITY: Belongs to the sigma-70 factor family.
 DR EMBL; AY422193; AAS90415.1; -;
 DR GO; GO:0016987; F:sigma factor activity; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006352; P:transcription initiation; IEA.
 DR InterPro; IPR007630; Sigma70_r4.
 DR InterPro; IPR000943; Sigma_70.
 DR Pfam; PF04545; Sigma70_r4; 1.
 DR PRINTS; PR00046; SIGMA70FCT.
 DR PROSITE; PS00716; SIGMA70_2; 1.
 DR DNA-binding; DNA-directed RNA polymerase; Sigma factor; Transcription;
 KW Transcription regulation; Transference.
 FT NON_TER 1
 SQ SEQUENCE 55 AA; 6365 MW; 7476036FCB12854 CRC64;
 Query Match 13.8%; Score 57; DB 2; Length 55;
 Best Local Similarity 39.0%; Pred. No. 1.3e+02;
 Matches 23; Conservative 3; Mismatches 15; Indels 18; Gaps 3;
 Qy 14 VRTGLGREAE---IEAVEVEIG-----FRDQYEMLRWRQQPAGLGVYAALERMGL 65
 Db 1 VRRFGLRGHESCTLEEVQGEIGLTRVRQIQVEALKRLRE-----ILEKNGL 48

RESULT 3
 Q7P321 PRELIMINARY; PRT; 59 AA.
 AC Q7P321;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Virulence-associated protein 1.
 GN Name=FN0340;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 OC NCBI_TaxID=209882;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49256;
 RA Karpatal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haeelkorn R., Overbeek R., Kyrpides N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AABF0100154; EAA23321.1; -;
 DR SEQUENCE 59 AA; 6808 MW; 615C5DF19B318E86 CRC64;
 SQ SEQUENCE 59 AA; 6808 MW; 615C5DF19B318E86 CRC64;
 Query Match 13.2%; Score 54.5; DB 2; Length 59;
 Best Local Similarity 37.2%; Pred. No. 2.6e+02;
 Matches 16; Conservative 5; Mismatches 21; Indels 1; Gaps 1;
 Qy 11 KEFVRTGLGREAEIEA-VEVEIGFRDQYEMLRWRQQPAG 52
 Db 9 KGMVOLLGLPEKEITALINAEISISHDIMYRIVKTMHQKNYG 51

RESULT 4
 Q9ZXL9 PRELIMINARY; PRT; 69 AA.
 AC Q9ZXL9;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Pseudomonas aeruginosa phage phi CTX, complete genome sequence.
 OS Bacteriophage phi CTX.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC P2-like viruses.
 OC NCBI_TaxID=35343;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=phiCTX-c;
 RX MEDLINE=90014160; PubMed=2507866;
 RA Hayaashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;
 RT "Pseudomonas aeruginosa cytotoxin: the nucleotide sequence of the gene
 and the mechanism of activation of the protoxin.";
 RL Mol. Microbiol. 31:399-419(1999).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=phiCTX-c;
 RX MEDLINE=99157549; PubMed=10027959;
 RA Nakayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayaashi T.;
 RT "The complete nucleotide sequence of phiCTX, a cytotoxin-converting
 phage of Pseudomonas aeruginosa: implications for phage evolution and
 horizontal gene transfer via bacteriophage.";
 RL Mol. Microbiol. 31:399-419(1999).
 DR EMBL; AB008550; BAA36234.1; -;
 DR InterPro; IPR008861; Tail_X.
 DR Pfam; PF05489; Phage_tail_X; 1.
 SQ SEQUENCE 69 AA; 7436 MW; D2E35A698F195CC0 CRC64;
 Query Match 13.1%; Score 54; DB 2; Length 69;
 Best Local Similarity 45.8%; Pred. No. 3.5e+02;
 Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 Qy 3 DAVPARRWKEFVRTLGLGREAEIEA 26
 Db 10 DTVEALCWRHYGRTAGVTAEVLEA 33

RESULT 5
 Q6CZU0 PRELIMINARY; PRT; 78 AA.
 AC Q6CZU0;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocuNames=ECA4061;
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OC NCBI_TaxID=29471;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Atkin R., Bacon N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagers K., Moule S., Norbertczak H.,
 RA Armond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
 RT "Genome sequence of the enterobacterial phytopathogen Erwinia
 carotovora subsp. atroseptica and characterization of virulence
 factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
 DR EMBL; BX950851; CAG76958.1; -;

```
DR InterPro; IPR008227; UCP006169.
DR InterPro; IPR010648; UPF0270.
DR Pfam; PF06794; UPF0270; 1.
DR PIRSF; PIRSF006169; UCP006169; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 78 AA; 8894 MW; CC29D8DC6F12BF9C CRC64;

Query Match 13.1%; Score 54; DB 2; Length 78;
Best Local Similarity 36.0%; Pred. No. 4e+02;
Matches 18; Conservative 4; Mismatches 16; Indels 12; Gaps 2;

Qy 41 MLKWRQOOPAGL-----GAVYAAERMGDCGVDSRLQRG 79
Db 1 MIIPQQLDPTLDSIIESFVLREGTDYGEQER-SLAQKVEDIRSLQSG 49

RESULT 6
Q8TYA5 PRELIMINARY; PRT; 79 AA.
ID Q8TYA5
AC Q8TYA5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted RNA-binding protein containing the S4 domain.
DE OrderedLocusNames=MK0398;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyzi; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OC NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezhevaeva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.I., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
RP "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
DR EMBL; AE010336; AAM01613.1; -
DR GO; GO:0003723; rRNA binding; IEA.
DR Pfam; PF01479; S4; 1.
DR SMART; SM00363; S4; 1.
DR PROSITE; PS00889; S4; 1.
KW Complete proteome.
SQ SEQUENCE 79 AA; 8930 MW; 87B143AA16BAF785 CRC64;

Query Match 13.0%; Score 53.5; DB 2; Length 79;
Best Local Similarity 32.4%; Pred. No. 4.6e+02;
Matches 22; Conservative 7; Mismatches 26; Indels 13; Gaps 3;

Qy 8 RWKFEVFTGLGREAIEAVE-VEIGRPDQOYEMLKWRQOOPAGLVAVYAAERMG 66
Db 5 RLDDAFLDVGVLAESEARRKRLVSGRVNGKLVKPKWLVSPG-----DEIEVD 55

Qy 67 GC---VED 71
Db 56 GVTVRVED 63

RESULT 7
Q72GH9 PRELIMINARY; PRT; 62 AA.
ID Q72GH9
AC Q72GH9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE OrderedLocusNames=TTIC1869;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.

OK NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wiezer A., Hartach T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacob C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus."
RL Nat. Biotechnol. 22:547-553 (2004).
DR EMBL; AE017307; AAS82211.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7921 MW; 0D272F18D427D6EA CRC64;

Query Match 12.8%; Score 53; DB 2; Length 62;
Best Local Similarity 29.3%; Pred. No. 4e+02;
Matches 17; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

Qy 8 RWKFEVFTGLGREAIEA-VEVEIGRPDQOYEMLKWRQOOPAGLVAVYAAERMG 64
Db 4 RRLKSVESYQARIREHQAKIEELRR-PEPRWELIRYWEKEIRTYPGRVERLLRRMG 60

RESULT 8
Q8U397 PRELIMINARY; PRT; 75 AA.
ID Q8U397
AC Q8U397;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PF0573.
DE OrderedLocusNames=PF0573;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OC NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VCI / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010180; AAL80697.1; -
DR Pfam; PF04014; SpoVT_AbrB; 1.
DR TIGRFAMs; TIGR01439; lp_hug_hel_AbrB; 1.
KW Complete proteome.
SQ SEQUENCE 75 AA; 8705 MW; 6FE2F4AF7D807146 CRC64;

Query Match 12.8%; Score 53; DB 2; Length 75;
Best Local Similarity 28.6%; Pred. No. 4.9e+02;
Matches 20; Conservative 14; Mismatches 24; Indels 12; Gaps 4;

Qy 5 VPARRWKEVFTGLGREAIEA-VEVEIGRPDQOYEMLKWRQOOPAG----LGAVYAAAL 60
Db 14 IPA----EIRKALGIGKEGELLEVRLENGKI---IIRLUKRRKTKLKUGKUTLEIEKAI 66

Qy 61 ERMGLDGCVE 70
Db 67 EE-GMKQCMQ 75

RESULT 9
Q7U9X2 PRELIMINARY; PRT; 78 AA.
ID Q7U9X2
AC Q7U9X2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE OrderedLocusNames=SYNW0130;
OS Synecchococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
```


QY 17 LGLREAEIEAIVEIGRFDQOYEMLEKRWQOOPAGLGAIVAAALERMG 64
DB 23 VGLRQGDKAVEVAINALHDSIQNVNK--NEIAQVGSISAADBEIG 67

RESULT 13

ID Q93NF5 PRELIMINARY; PRT; 70 AA.
AC Q93NF5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE ORP70 (Hypothetical protein).
OS Arthrobacter nicotinovorans.
OS Plasmid pAO1, and Plasmid pAO1.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=29320;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=pAO1, and pAO1;
RX MEDLINE=21405725; PubMed=11514508;
RX DOI=10.1128/JB.183.18.5262-5267.2001;
RA Baitsch D., Sandu C., Brandsch R., Igloi G.L.;
RT "Gene cluster on pAO1 of Arthrobacter nicotinovorans involved in
RT degradation of the plant alkaloid nicotine: cloning, purification, and
RT characterization of 2,6-dihydroxypyridine 3-hydroxylase.";
RL J. Bacteriol. 183:5262-5267(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC PLASMID=pAO1;
RX MEDLINE=95115562; PubMed=7815950;
RA Grether-Beck S., Igloi G.L., Fust S., Schiltz E., Decker K.,
RA Brandsch R.;
RT "Structural analysis and molybdenum-dependent expression of the pAO1-
RT encoded nicotine dehydrogenase genes of Arthrobacter nicotinovorans";
RL Mol. Microbiol. 13:929-936(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC PLASMID=pAO1;
RX MEDLINE=96172783; PubMed=8588735;
RA Menendez C., Igloi G., Henninger H., Brandsch R.;
RT "A pAO1-encoded molybdopterin cofactor gene (moaA) of Arthrobacter
RT nicotinovorans: characterization and site-directed mutagenesis of the
RT encoded protein.";
RL Arch. Microbiol. 164:142-151(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC PLASMID=pAO1;
RX MEDLINE=98089892; PubMed=9428706;
RA Menendez C., Otto A., Igloi G., Nick P., Brandsch R., Schubach B.,
RA Bottcher B., Brandsch R.;
RT "Molybdate-uptake genes and molybdopterin-biosynthesis genes on a
RT bacterial plasmid. Characterization of MoaA as a filament-forming
RT protein with adenosinetriphosphatase activity.";
RL Eur. J. Biochem. 250:524-531(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC PLASMID=pAO1;
RX MEDLINE=9906870; PubMed=9878353; DOI=10.1006/jmbi.1998.2227;
RA Schenk S., Hoelz A., Kraus B., Decker K.;
RT "Gene structure and properties of enzymes of the plasmid-encoded
RT nicotine catabolism of Arthrobacter nicotinovorans.";
RL J. Mol. Biol. 284:1323-1339(1998).
RN [6]
RP SEQUENCE FROM N.A.
RC PLASMID=pAO1;
RX MEDLINE=97230479; PubMed=9073580; DOI=10.1006/plas.1996.1272;
RA Menendez C., Igloi G.L., Brandsch R.;
RT "IS1473, a putative insertion sequence identified in the plasmid pAO1
RT from Arthrobacter nicotinovorans: isolation, characterisation and
RT distribution among Arthrobacter species.";
RL Plasmid 37:35-41(1997).

[7]
RP SEQUENCE FROM N.A.
RC PLASMID=pAO1;
RX MEDLINE=22505657; PubMed=12618462;
RX DOI=10.1128/JB.185.6.1976-1986.2003;
RA Igloi G.L., Brandsch R.;
RT "Sequence of the 16S-kilobase catabolic plasmid pAO1 from Arthrobacter
RT nicotinovorans and identification of a pAO1-dependent nicotine uptake
RT system.";
RL J. Bacteriol. 185:1976-1986(2003).
DR EMBL; AF373840; AAK64270.1; -;
DR EMBL; AJ507836; CAD47929.1; -;
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 70 AA; 7833 MW; 1501DDE147F444FF CRC64;
Query Match 12.6%; Score 52; DB 2; Length 70;
Best Local Similarity 36.6%; Pred. No. 5.8e+02;
Matches 15; Conservative 3; Mismatches 23; Indels 0; Gaps 0;
QY 35 RDQYEMLEKRWQOOPAGLGAIVAAALERMGLDGCVEDLRSR 75
DB 30 RDDQMTWLGRTDLPPSGGLGCAADTKGGRCLCVNKSCHR 70
RESULT 14
Q88AU2
ID Q88AU2 PRELIMINARY; PRT; 66 AA.
AC Q88AU2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PSPTO0294;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.F., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AE016857; AA053839.1; -;
DR TIGR; PSPTO0294; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 66 AA; 7274 MW; 6DD44F84FA4A630C CRC64;

Query Match 12.3%; Score 51; DB 2; Length 66;

Best Local Similarity 46.2%; Pred. No. 7e+02;
Matches 12; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 54 GAVYAALERMGLDGCVEDLRSRLQRG 79
DB 29 GAVATAFEKALDQMTADARRALQRG 54

RESULT 15

Q7EYN4
ID Q7EYN4 PRELIMINARY; PRT; 63 AA.
AC Q7EYN4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

Search completed: June 27, 2005, 14:40:56
Job time : 174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:22:33 ; Search time 158 Seconds
(without alignments)
195.828 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVRTTLGLR.....ERMGLDGCVEDLRSLRQGP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1092469

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	92.3	74	5	ABG31492 Human Apo
2	381	92.3	74	7	ADG98744 Apo-3/DR3
3	381	92.3	74	8	ADO40453 Human Apo
4	338	81.8	65	2	AAW93610 Human DR3
5	338	81.8	65	3	AB266990 Human DR3
6	155	37.5	78	5	ABG31493 Human Apo
7	155	37.5	78	6	ADA49709 Death dom
8	155	37.5	78	7	ADG98745 TNFR1 dea
9	155	37.5	78	8	ADO40454 Human TNF
10	142	34.4	69	2	AAW93612 Human TNF
11	139	33.7	30	4	AAO08695 Human Pol
12	136.5	33.1	68	3	AB266989 Human TNF
13	118	28.6	64	2	AAW00208 Human p55
14	105	25.4	75	7	ADG42594 NOV1 doma
15	94	22.8	76	8	ADO40451 Human Apo
16	83	20.1	67	3	AB266992 Human DR5
17	82	19.9	67	2	AAW93613 Human CAR
18	77.5	18.8	67	3	AAV67948 Tumour ne
19	74	17.9	45	4	AAW89832 Human imm
20	74	17.9	76	7	ADG98743 DR4 death
21	74	17.9	76	8	ADO40452 Human DR4
22	70.5	17.1	77	6	ADA49713 Death dom
23	68	16.5	67	3	AB266991 Human DR4
24	67	16.2	51	2	AB266985 Partial h
25	64.5	15.6	65	5	AAE24868 Chlamydia

26	64.5	15.6	65	5	AAE38911	Aae38911 Chlamydia
27	60	14.5	77	2	AAW62177	Aaw62177 Nerve gro
28	60	14.5	77	8	ADJ25858	Adj25858 Nerve gro
29	57.5	13.9	63	2	AAW00206	Aaw00206 Human Fas
30	57.5	13.9	68	2	AAW93611	Aaw93611 Human Fas
31	57.5	13.9	68	3	AB266988	Ab266988 Human CD9
32	57.5	13.9	68	4	AAW80357	Aaw80357 Human hae
33	57.5	13.9	77	5	ABG31494	Abg31494 Human Apo
34	57.5	13.9	77	6	ADA49710	Ada49710 Death dom
35	57.5	13.9	77	7	ADG98746	Adg98746 Fas/Apo1
36	57.5	13.9	77	8	ADO40455	Ado40455 Human Fas
37	57	13.8	65	5	AAE24866	Aae24866 Chlamydia
38	57	13.8	65	5	AAE38909	Aae38909 Chlamydia
39	57	13.8	71	5	AAE24857	Aae24857 Mouse NGF
40	57	13.8	71	5	AAE38900	Aae38900 Mouse NGF
41	56.5	13.7	73	8	ADN46273	Adn46273 Thermococ
42	56	13.6	65	5	AAE24856	Aae24856 Chlamydia
43	56	13.6	65	5	AAE38899	Aae38899 Chlamydia
44	55	13.3	60	4	AAU63529	Aau63529 Propionib
45	55	13.3	60	6	ABM60048	Abm60048 Propionib

ALIGNMENTS

RESULT 1
ABG31492
ID ABG31492 standard; protein; 74 AA.
XX
AC ABG31492;
XX
XX 21-NOV-2002 (first entry)
XX
DE Human Apo-2DcR associated protein #2.
XX
KW Human; Apo-2DcR; Apo-2 ligand; programmed cell death; apoptosis;
KW neurodegenerative disease; autoimmune; inflammatory.
XX
OS Homo sapiens.
XX
PN US2002102706-A1.
XX
PD 01-AUG-2002.
XX
PF 21-JUN-2001; 2001US-00887879.
XX
PR 18-JUN-1997; 97US-0049911P.
PR 12-JUN-1998; 98US-00096500.
XX
(GETH) GENENTECH INC.
XX
Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A, Kim KJ;
Wood WI;
XX
WPI; 2002-697823/75.
XX
Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in
mammalian cells.
XX
Disclosure; Page 37; 58pp; English.

The present invention relates to the isolation of novel human polypeptides, designated Apo-2DcR, and the polynucleotide sequences encoding them. Apo-2DcR is capable of binding Apo-2 ligand and is useful for modulating programmed cell death or apoptosis in mammalian cells. Apo-2DcR can be used to produce apo-2DcR antibodies which are useful therapeutically, and can cross-react with other receptors for Apo-2 ligand to block excessive apoptosis in neurodegenerative diseases, or to block potentially autoimmune or inflammatory effects. Apo-2DcR antibodies are also useful in immunohistochemistry staining assays or diagnostic assays for Apo-2DcR, e.g. detecting it's expression in specific cells, tissues or serum, and for the affinity purification of Apo-2DcR from recombinant cell culture or natural sources. The present sequence

XX 18-JUN-1999 (first entry)
XX Human DR3 protein fragment.
XX Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;
KW p53-inducible; apoptosis-mediating activity; treatment; animal model;
KW neoplastic disease; DR3.
XX
XX Homo sapiens.
XX WO9502653-A1.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US014495.
XX
XX 11-JUL-1997; 97US-0052305P.
PR 04-AUG-1997; 97US-0054710P.
PR 30-SEP-1997; 97US-0060473P.
PR 11-MAR-1998; 98US-0077526P.
PR 11-MAR-1998; 98US-0077628P.
PR 11-MAR-1998; 98US-0077661P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX El-Deiry WS;
XX
XX WPI; 1999-120857/10.
XX
XX A new nucleic acid encodes a p53-induced protein (Killer) - which induces
PT apoptosis and is useful in the diagnosis and treatment of neoplastic
PT diseases.
XX
XX Disclosure; Page 46; 65pp; English.
XX This invention describes a novel human adriamycin-inducible killer
CC protein located on chromosome 8p21, which also has p53-inducible,
CC apoptosis-mediating activity and comprises an amino-terminal
CC extracellular receptor, transmembrane and death domains. The nucleic acid
CC molecule which encodes the protein, it's encoded signal transduction
CC protein and antibodies of the invention are useful in the diagnosis and
CC treatment of neoplastic diseases. The invention is also useful for the
CC production of animal model systems
XX
XX Sequence 65 AA;
Query Match 81.8%; Score 338; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 60
QY 69 VEDLR 73
Db 61 VEDLR 65
RESULT 5
AAB26990
ID AAB26990 standard; protein; 65 AA.
XX
XX AAB26990;
XX
XX 02-FEB-2001 (first entry)
XX Human DR3 death domain.
XX Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
XX

KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data;
XX osteoprotegerin; DR3.
XX
XX Homo sapiens.
XX WO200056862-A1.
XX
XX 28-SEP-2000.
XX
XX 16-MAR-2000; 2000WO-US006831.
XX
XX 24-MAR-1999; 99US-0126019P.
PR 14-MAY-1999; 99US-0134220P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Gentz RL, Yu G, Fan P;
XX WPI; 2000-594575/56.
XX
XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer.
XX
XX Disclosure; Fig 4C; 220pp; English.
XX
XX The present sequence is the death domain of DR3. It was used for
CC comparison to a domain of a novel human tumour necrosis factor receptor,
CC designated TR9. The TR9 receptor is also known as Death Domain Containing
CC Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for
CC treating, preventing or diagnosing common variable immunodeficiency, X-
CC linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-
CC Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis,
CC allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and
CC asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and
XX other neurological diseases
XX
XX Sequence 65 AA;
Query Match 81.8%; Score 338; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLREAEIEAVEVEIGRFRDQYEMLKRWQQQPAGLGAVYAALERMGLDGC 60
QY 69 VEDLR 73
Db 61 VEDLR 65
RESULT 6
ABG31493
ID ABG31493 standard; protein; 78 AA.
XX
XX ABG31493;
XX
XX 21-NOV-2002 (first entry)
XX Human Apo-2DcR associated protein #3.
XX Human; Apo-2DcR; Apo-2 ligand; programmed cell death; apoptosis;
KW neurodegenerative disease; autoimmune; inflammatory.
XX
XX Homo sapiens.
XX

PN US2002102706-A1.
XX 01-AUG-2002.
XX 21-JUN-2001; 2001US-00887879.
XX 18-JUN-1997; 97US-0049911P.
PR 12-JUN-1998; 98US-00096500.
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A, Kim KJ;
PI Wood WJ;
XX WPI; 2002-697823/75.
XX Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in
PT mammalian cells.
XX Disclosure; Page 37; 58pp; English.
XX The present invention relates to the isolation of novel human
CC polypeptides, designated Apo-2DcR, and the polynucleotide sequences
CC encoding them. Apo-2DcR is capable of binding Apo-2 ligand and is useful
CC for modulating programmed cell death or apoptosis in mammalian cells. Apo
CC -2DcR can be used to produce apo-2DcR antibodies which are useful
CC therapeutically, and can cross-react with other receptors for Apo-2
CC ligand to block excessive apoptosis in neurodegenerative diseases, or to
CC block potentially autoimmune or inflammatory effects. Apo-2DcR antibodies
CC are also useful in immunohistochemistry staining assays or diagnostic
CC assays for Apo-2DcR, e.g. detecting it's expression in specific cells,
CC tissues or serum, and for the affinity purification of Apo-2DcR from
CC recombinant cell culture or natural sources. The present sequence
CC represents a protein of unknown function relating to the present
CC invention. Note: The present sequence is given in the Seq listing but is
CC not mentioned elsewhere in the specification
XX
SQ Sequence 78 AA;
Query Match 37.5%; Score 155; DB 5; Length 78;
Best Local Similarity 46.1%; Pred. No. 7e-12; Indels 4; Gaps 2;
Matches 35; Conservative 13; Mismatches 24;
QY 1 VMDAVPARRWKEFVRTGLGREAEIEAVEVEIGR-FRDQQYEMLKRWQQQP---AGLGAV 56
Db 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
Db 61 GRVLRDMDLLGCLEDI 76
RESULT 7
ADA49709
ID ADA49709 standard; protein; 78 AA.
XX ADA49709;
XX 20-NOV-2003 (first entry)
DE Death domain of human TNFR1 (htnfr1) protein.
XX Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;
KW competitive-type receptor; binding assay; cancer cell; human;
KW TNF receptor family; htnfr1; death domain; cytostatic.
XX Homo sapiens.
OS US2002192729-A1.
PN 19-DEC-2002.
XX 28-MAR-2002; 2002US-00112793.
PF

XX 01-APR-1996; 96US-00625328.
PR 23-SEP-1996; 96US-00710802.
PR 31-MAR-1997; 97US-00828683.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
PI WPI; 2003-657226/62.
XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
PT Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
PT in diagnostic assays.
XX Disclosure; Fig 6; 53pp; English.
XX The present invention relates to the isolation of a biologically active
CC Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polynucleotide
CC sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The
CC Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI
CC is useful for generating antibodies, as standards in assays for Apo-3 or
CC Apo-2LI, in affinity purification techniques, and in competitive-type
CC receptor binding assays when labelled with radioiodine, enzymes or
CC fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
CC inducing apoptosis in cancer cells, and thus have therapeutic utility.
CC The present sequence represents the death domain of a human TNF receptor
CC family protein. This sequence is compared with the death domain of human
CC Apo-3.
XX
SQ Sequence 78 AA;
Query Match 37.5%; Score 155; DB 6; Length 78;
Best Local Similarity 46.1%; Pred. No. 7e-12; Indels 4; Gaps 2;
Matches 35; Conservative 13; Mismatches 24;
QY 1 VMDAVPARRWKEFVRTGLGREAEIEAVEVEIGR-FRDQQYEMLKRWQQQP---AGLGAV 56
Db 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLREAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
Db 61 GRVLRDMDLLGCLEDI 76
RESULT 8
ADG98745
ID ADG98745 standard; protein; 78 AA.
XX ADG98745;
XX 11-MAR-2004 (first entry)
DE TNFR1 death domain protein.
XX Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
KW cancer; gene therapy.
XX Unidentified.
OS US2003148455-A1.
PN 07-AUG-2003.
XX 06-NOV-2002; 2002US-00288917.
XX 15-MAY-1997; 97US-0046615P.
PR 09-FEB-1998; 98US-0074119P.
PR 14-MAY-1998; 98US-00079029.
PR 02-NOV-2001; 2001US-00052798.
XX (GETH) GENENTECH INC.
XX

PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI; 2003-897574/82.
XX New Apo-2 polypeptide or its extracellular or death domain sequence,
XX useful for modulating apoptosis in mammalian cancer cells or for
XX generating transgenic or knockout animals.
XX Disclosure; Fig 2B; 64pp; English.
XX The present invention provides novel Apo-2 protein and the nucleic acid
XX encoding the protein. The invention is useful in inducing apoptosis in
XX mammalian cancer cells. The invention is also useful in diagnostic
XX procedures for tissue-specific typing and in generating transgenic
XX animals that are useful in development and screening of reagents. The
XX invention is also useful in gene therapy. The present sequence is TNFR1
XX (tumour necrosis factor receptor 1) death domain protein.
XX Sequence 78 AA;
SQ

Query Match 37.5%; Score 155; DB 7; Length 78;
Best Local Similarity 46.1%; Pred. No. 7e-12;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRLTGLREAEIIEVEIGR-FRQOQYEMLKRWQQQP---AGLCGV 56
Db 1 VVENVPLRWKEFVRLTGLREAEIIEVEIGR-FRQOQYEMLKRWQQQP---AGLCGV 56
QY 57 YAALERMGLDGCVEDL 72
Db 61 GRVLRLDMLLGLEDI 76

RESULT 9
ADO40454
ID ADO40454 standard; protein; 78 AA.
XX ADO40454;
XX 15-JUL-2004 (first entry)
XX Human TNFR1 protein.
XX Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;
XX gene therapy; human; TNFR1; receptor.
XX Homo sapiens.
XX US2004009552-A1.
XX 15-JAN-2004.
XX 25-APR-2003; 2003US-00423448.
XX 15-MAY-1997; 97US-0046615P.
XX 09-FEB-1998; 98US-0074119P.
XX 14-MAY-1998; 98US-00079029.
XX 02-NOV-2001; 2001US-00052798.
XX 06-NOV-2002; 2002US-00288917.
XX (GETH) GENENTECH INC.
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI; 2004-090468/09.
XX New Apo-2 polypeptides and encoding nucleic acid molecules, useful for
XX diagnosing, preventing or treating cancer, and in tissue typing or in
XX generating antibodies or transgenic animals.
XX Example 1; Fig 2B; 53pp; English.
XX The present invention provides novel Apo-2 polypeptide and the encoding

CC polynucleotide capable of modulating apoptosis. The invention is useful
CC in diagnosing, treating and preventing cancer, tissue typing, in
CC generating antibodies and transgenic animals. The invention is also
CC useful in gene therapy. The present sequence is human TNFR1 protein. This
CC sequence is used in the exemplification of the invention
XX Sequence 78 AA;
SQ

Query Match 37.5%; Score 155; DB 8; Length 78;
Best Local Similarity 46.1%; Pred. No. 7e-12;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRLTGLREAEIIEVEIGR-FRQOQYEMLKRWQQQP---AGLCGV 56
Db 1 VVENVPLRWKEFVRLTGLREAEIIEVEIGR-FRQOQYEMLKRWQQQP---AGLCGV 56
QY 57 YAALERMGLDGCVEDL 72
Db 61 GRVLRLDMLLGLEDI 76

RESULT 10
AAW93612
ID AAW93612 standard; protein; 69 AA.
XX AAW93612;
XX 18-JUN-1999 (first entry)
XX Human TNFR-1 protein fragment.
XX Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;
XX p53-inducible; apoptosis-mediating activity; treatment; animal model;
XX neoplastic disease; TNFR-1.
XX Homo sapiens.
XX WO9902653-A1.
XX 21-JAN-1999.
XX 10-JUL-1998; 98WO-US014495.
XX 11-JUL-1997; 97US-0052305P.
XX 04-AUG-1997; 97US-0054710P.
XX 30-SEP-1997; 97US-0060473P.
XX 11-MAR-1998; 98US-0077526P.
XX 11-MAR-1998; 98US-0077628P.
XX 11-MAR-1998; 98US-0077661P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX El-Deiry WS;
XX WPI; 1999-120857/10.
XX A new nucleic acid encodes a p53-induced protein (Killer) - which induces
XX apoptosis and is useful in the diagnosis and treatment of neoplastic
XX diseases.
XX Disclosure; Page 46; 65pp; English.
XX This invention describes a novel human adriamycin-inducible killer
XX protein located on chromosome 8p21, which also has p53-inducible,
XX apoptosis-mediating activity and comprises an amino-terminal
XX extracellular receptor, transmembrane and death domains. The nucleic acid
XX molecule which encodes the protein, it's encoded signal transduction
XX protein and antibodies of the invention are useful in the diagnosis and
XX treatment of neoplastic diseases. The invention is also useful for the
XX production of animal model systems
XX Sequence 69 AA;
SQ

```
Query Match      34.4%; Score 142; DB 2; Length 69;
Best Local Similarity 47.1%; Pred. No. 2.8e-10;
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

QY 9 RWKEFVRTLGLREARIEAVEVEIGR-FRDOQYEMLKRWQOOP---AGLGAVYAALERMG 64
DB 1 RWKEFVRTLGLSDHEIDRLQNGRCLEAQYSLMATWRRTRTREATLELLGRVLRDMD 60

QY 65 LDGCVEDL 72
DB 61 LGCLEDI 68

RESULT 11
AAO08695
ID AAO08695 standard; protein; 30 AA.
XX
AC AAO08695;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 22587.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
FN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US004927.
XX
PR 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
DR N-PSDB; AAI88626.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
PS Claim 20; SEQ ID NO 22587; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 30 AA;

Query Match      33.7%; Score 139; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 GAVYAALERMGLDGCVEDLRSRLQGP 80
DB 54 GAVYAALERMGLDGCVEDLRSRLQGP 80
```

```
Db 4 GAVYAALERMGLDGCVEDLRSRLQGP 30

RESULT 12
AAB26989
ID AAB26989 standard; protein; 68 AA.
XX
AC AAB26989;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human TNFR 1 death domain.
XX
KW Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiac; antiasthmatic; antidiabetic; antiallergic;
KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data;
KW osteoprotegerin; TNFR 1.
XX
OS Homo sapiens.
XX
FN WO2000056862-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US006831.
XX
PR 24-MAR-1999; 99US-0126019P.
PR 14-MAY-1999; 99US-0134220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Gentz RL, Yu G, Fan P;
XX
DR WPI; 2000-594575/56.
XX
PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer.
XX
PS Disclosure; Fig 4C; 220pp; English.
XX
CC The present sequence is the death domain of TNFR 1. It was used for
CC comparison to a domain of a novel human tumour necrosis factor receptor,
CC designated TR9. The TR9 receptor is also known as Death Domain Containing
CC Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for
CC treating, preventing or diagnosing common variable immunodeficiency, X-
CC linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-
CC Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis,
CC allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and
CC asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and
CC other neurological diseases
XX
SQ Sequence 68 AA;

Query Match      33.1%; Score 136.5; DB 3; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.4e-09;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVRTLGLREARIEAVEVEIGR-FRDOQYEMLKRWQO--QQPAGLGAVYAALERMGL 65
DB 1 RWKEFVRTLGLSDHEIDRLQNGRCLEAQYSLMATWRRTRTREATLELLGRVLRDMDL 60

QY 66 DGCVEDL 72
DB 61 LGCLEDI 67
```



```
RESULT 13
AAW00208
ID AAW00208 standard; peptide; 64 AA.
XX
XX
AC AAW00208;
XX
DT 16-APR-1997 (first entry)
XX
DE Human p55 tumour necrosis factor receptor death domain motif.
XX
KW Death domain; regulatory protein; NGF-R; nerve growth receptor; FAS-R;
KW Fas ligand receptor; Fas/AF01; ankyrin 1; p55 TNF-R;
KW tumour necrosis factor receptor; MORT1; cell cytotoxicity; HIV;
KW human immunodeficiency virus; cancer; neoplasia; disease.
XX
OS Homo sapiens.
XX
PN WO9625941-A1.
XX
PD 29-AUG-1996.
XX
PF 15-FEB-1996; 96WO-US002326.
XX
PR 22-FEB-1995; 95IL-00112742.
PR 13-SEP-1995; 95IL-00115289.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
PA (WEIN/) WEINURZEL H.
XX
PI Wallach D, Boldin MP, Varfolomeev EE, Pancer Z, Mett I;
PI Goncharov TM;
XX
DR WPI; 1996-402125/40.
XX
PT Modulator of regulatory cellular events mediated by "death domain" contg.
PT regulatory proteins - useful for modulating functions mediated in cells
PT by proteins contg the death domain.
XX
PS Claim 9; Fig 1; 74pp; English.
XX
CC AAW00207 shows the death domain of the p55 tumour necrosis factor
CC receptor (p55 TNF-R). The death domain (DD) of human Fas-ligand receptor
CC (FAS-R), ankyrin 1, nerve growth factor receptor (NGF-R) and MORT-1
CC (which binds to the intracellular portion of (FAS-R)) are also given (see
CC AAW00206-07 and AAW00209-W00210). These DDs are used to identify
CC compounds capable of modulating activity of the regulatory proteins (p55,
CC NGF, TNF and FAS-R ligand, MORT-1) via interaction with the DDs. Such
CC modulators which may be antibodies, antisense sequences or ribozymes
CC (which can affect the cellular mRNA sequences encoding the proteins) and
CC are useful for modulation of effects of the regulatory proteins within
CC the cell. Tumour cells, HIV-infected cells or other diseased cells can be
CC treated by targeting the cells with animal viral vectors encoding the
CC modulators and a viral surface antigen capable of binding to a specific
CC receptor. The DDs are characterised by having groups of common amino acid
CC residues Trp, Ala, Asp, Glu, Thr, Arg and Tyr within locations that can
CC be aligned to show homology
XX
SQ Sequence 64 AA;
Query Match 28.6%; Score 118; DB 2; Length 64;
Best Local Similarity 42.6%; Pred. NO. 3.2e-07;
Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;
Oy 10 WKFEVRLGLRAEAEVEVEIGR-FRDOQYEMLRKRWQOQAPAGLGVAYVALERMG----64
Db 1 WKFEVRLGLSDHEIDRLQNGRLCRAQYSLMATWRRTRPR-----EATLELGRVLR 56
Oy 65 ---LDGCV 69
Db 57 DHDLGLCL 64
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```
RESULT 14
ADG42594
ID ADG42594 standard; protein; 75 AA.
XX
XX
AC ADG42594;
XX
DT 26-FEB-2004 (first entry)
XX
DE NOV1 domain analysis associated protein seq id 47.
XX
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
KW NOVX-associated disorder; cancer; NOVX; domain analysis.
XX
OS Unidentified.
XX
PN US2003204052-A1.
XX
PD 30-OCT-2003.
XX
PF 04-OCT-2001; 2001US-00970944.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (HERR/) HERRMANN J L.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2003-900673/82.
XX
PT New NOVX gene or NOVX-specific antibody, useful for preparing a
PT composition for treating or preventing a NOVX-associated disorder, e.g.,
PT cancer.
XX
PS Disclosure; SEQ ID NO 47; 118pp; English.
XX
CC The invention describes a new isolated polypeptide comprising: a
CC polypeptide or its mature form comprising a sequence not given in the
CC specification; or a variant of (A), where one or more amino acid residues
CC in the variant differs in no more than 15% from the amino acid sequence
CC of the mature form. The pharmaceutical composition may be administered
CC via oral, transdermal, rectal or parenteral route. The polypeptide,
CC nucleic acid or antibody is useful for preparing a composition for
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
CC the amino acid sequence of a protein associated with analysis of domains
CC in human NOV1 protein.
XX
SQ Sequence 75 AA;
Query Match 25.4%; Score 105; DB 7; Length 75;
Best Local Similarity 35.3%; Pred. No. 1.8e-05;
Matches 24; Conservative 12; Mismatches 30; Indels 2; Gaps 1;
Oy 1 VMDAVPARRWKEFVRTGLRRAEAEVEVEIGRFRDOQYEMLRKRWQO--OPAGLGVAY 58
Db 6 LLDDPLGRWRRLARKLGLSEEDIQIEHENPRLASPTYQLLDIWEQRGKNATVTGLE 65
Oy 59 ALERMGLD 66
Db 66 ALRMGRD 73
RESULT 15
ADO40451
ID ADO40451 standard; protein; 76 AA.
XX
XX
AC ADO40451;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human Apo-2 protein #2.
XX
```

KW Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;
KW gene therapy; human.
XX Homo sapiens.
OS
XX US2004009552-A1.
FN
XX
XX 15-JAN-2004.
PD
XX
XX 25-APR-2003; 2003US-00423448.
PF
XX
XX 15-MAY-1997; 97US-0046615P.
PR
PR 09-FEB-1998; 98US-0074119P.
PR 14-MAY-1998; 98US-00079029.
PR 02-NOV-2001; 2001US-00052798.
PR 06-NOV-2002; 2002US-00288917.
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
PI
XX WPI; 2004-090468/09.
DR
XX
XX New Apo-2 polypeptides and encoding nucleic acid molecules, useful for
PT diagnosing, preventing or treating cancer, and in tissue typing or in
PT generating antibodies or transgenic animals.
XX
XX Example 1; SEQ ID NO 14; 53pp; English.
PS
XX
XX The present invention provides novel Apo-2 polypeptide and the encoding
CC polynucleotide capable of modulating apoptosis. The invention is useful
CC in diagnosing, treating and preventing cancer, tissue typing, in
CC generating antibodies and transgenic animals. The invention is also
CC useful in gene therapy. The present sequence is human Apo-2 protein. This
CC sequence is used in the exemplification of the invention
XX
XX Sequence 76 AA;
SQ
Query Match 22.8%; Score 94; DB 8; Length 76;
Best Local Similarity 34.4%; Pred. No. 0.00049;
Matches 22; Conservative 11; Mismatches 29; Indels 2; Gaps 1;
Qy 3 DAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOYEMLKRW--RQQQPAGLGAVYAAL 60
Db 3 DLVFPDSWEPLMRKGLGLMDNEIKVAKAEAGHRDTLYTMLIKWVNTKGRDASVHTLLDAL 62
Qy 61 ERMG 64
Db 63 ETLG 66
Search completed: June 27, 2005, 14:37:58
Job time : 160 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2005, 14:38:10 ; Search time 163 Seconds
(without alignments)
188.735 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVRTIGLR.....ERMGLDGCVDLRRLRQGP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 666033

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	92.3	74	9	US-09-887-879-15
2	381	92.3	74	9	US-09-992-964-15
3	381	92.3	74	14	US-10-207-295-9
4	381	92.3	74	14	US-10-242-383-15
5	338	81.8	65	9	US-09-756-854-24
6	338	81.8	65	13	US-10-041-574-24
7	338	81.8	65	16	US-10-834-966-24
8	155	37.5	78	9	US-09-887-879-16
9	155	37.5	78	9	US-09-992-964-16
10	155	37.5	78	13	US-10-112-793-23
11	155	37.5	78	14	US-10-207-295-10
Sequence 15, Appl					
Sequence 15, Appl					
Sequence 9, Appl					
Sequence 15, Appl					
Sequence 24, Appl					
Sequence 24, Appl					
Sequence 16, Appl					
Sequence 16, Appl					
Sequence 16, Appl					
Sequence 23, Appl					

12	155	37.5	78	14	US-10-242-383-16	Sequence 16, Appl
13	136.5	33.1	68	9	US-09-756-854-23	Sequence 23, Appl
14	136.5	33.1	68	13	US-10-041-574-23	Sequence 23, Appl
15	136.5	33.1	68	16	US-10-834-966-23	Sequence 23, Appl
16	118	28.6	64	13	US-10-035-408-3	Sequence 3, Appl
17	94	22.8	76	14	US-10-207-295-7	Sequence 7, Appl
18	83	20.1	67	9	US-09-756-854-26	Sequence 26, Appl
19	83	20.1	67	13	US-10-041-574-26	Sequence 26, Appl
20	83	20.1	67	16	US-10-834-966-26	Sequence 26, Appl
21	74	17.9	76	14	US-10-207-295-8	Sequence 8, Appl
22	70.5	17.1	77	13	US-10-112-793-27	Sequence 7, Appl
23	70.5	17.1	77	14	US-10-287-594-7	Sequence 7, Appl
24	68	16.5	67	9	US-09-756-854-25	Sequence 25, Appl
25	68	16.5	67	13	US-10-041-574-25	Sequence 25, Appl
26	68	16.5	67	16	US-10-834-966-25	Sequence 25, Appl
27	64.5	15.6	65	14	US-10-001-254-56	Sequence 56, Appl
28	63	15.3	62	15	US-10-424-599-188281	Sequence 188281,
29	60	14.5	77	17	US-10-656-250-118	Sequence 118, App
30	57.5	13.9	63	13	US-10-035-408-1	Sequence 1, Appl
31	57.5	13.9	68	9	US-09-756-854-22	Sequence 22, Appl
32	57.5	13.9	68	9	US-09-796-692-721	Sequence 721, App
33	57.5	13.9	68	13	US-10-041-574-22	Sequence 22, App
34	57.5	13.9	68	14	US-10-040-862-721	Sequence 721, App
35	57.5	13.9	68	15	US-10-057-4758-721	Sequence 721, App
36	57.5	13.9	68	15	US-10-154-884B-721	Sequence 721, App
37	57.5	13.9	68	16	US-10-764-324-721	Sequence 721, App
38	57.5	13.9	68	16	US-10-834-966-22	Sequence 22, App
39	57.5	13.9	77	9	US-09-887-879-17	Sequence 17, Appl
40	57.5	13.9	77	9	US-09-992-964-17	Sequence 17, Appl
41	57.5	13.9	77	13	US-10-112-793-24	Sequence 24, Appl
42	57.5	13.9	77	14	US-10-207-295-11	Sequence 11, Appl
43	57.5	13.9	77	14	US-10-242-383-17	Sequence 17, Appl
44	57	13.8	60	16	US-10-437-963-139854	Sequence 139854,
45	57	13.8	65	14	US-10-001-254-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-09-887-879-15
; Sequence 15, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2dcr
; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-879-15

Query Match 92.3%; Score 381; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.2e-38; Indels 0; Gaps 0;
Matches 74; Conservative 0; Mismatches 0;

Oy 1 VMDAVPARRWKEFVRTIGLRRAEAEVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

Db 1 VMDAVPARRWKEFVRTIGLRRAEAEVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

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Qy 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 2
US-09-992-964-15
; Sequence 15, Application US/09992964
; Patent No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-964-15

Query Match 92.3%; Score 381; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRWKROOQPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRWKROOQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 3
US-10-207-295-9
; Sequence 9, Application US/10207295
; Publication No. US20030017161A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung Jin
; TITLE OF INVENTION: APO-2 RECEPTOR
; FILE REFERENCE: 11669.28US04
; CURRENT APPLICATION NUMBER: US/10/207,295
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/020,746
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 08/857,216
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-295-9

Query Match 92.3%; Score 381; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRWKROOQPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRWKROOQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74
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Db 61 ERMGLDGCVEDLRS 74

RESULT 4
US-10-242-383-15
; Sequence 15, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110P1
; CURRENT APPLICATION NUMBER: US/10/242,383
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/887,879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-383-15

Query Match 92.3%; Score 381; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMDAVPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRWKROOQPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRWKROOQPAGLGAVYAAL 60

Qy 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 5
US-09-756-854-24
; Sequence 24, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24

Query Match      81.8%; Score 338; DB 9; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 6
US-10-041-574-24
; Sequence 24, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-24

Query Match      81.8%; Score 338; DB 13; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 7
US-10-834-966-24
; Sequence 24, Application US/10834966
; Publication No. US20040197870A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/834,966
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-834-966-24

Query Match      81.8%; Score 338; DB 16; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 8
US-09-887-879-16
; Sequence 16, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
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Db 61 VEDLR 65

RESULT 7
US-10-834-966-24
; Sequence 24, Application US/10834966
; Publication No. US20040197870A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/834,966
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-834-966-24

Query Match      81.8%; Score 338; DB 16; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOYEMLKRWQQQPAGLGAVYAALERMGLDGC 60

Qy 69 VEDLR 73
|
Db 61 VEDLR 65

RESULT 8
US-09-887-879-16
; Sequence 16, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
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;
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
;
US-09-756-854-23

Query Match 33.1%; Score 136.5; DB 9; Length 68;
Best Local Similarity 46.3%; Pred. No. 7.7e-09;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps

QY 9 RWKEFVRTIGLREARTEAVEIGR-FRDOQVEMLKRWQ--QQPAGLGAVYAALERMGL 65
DB 1 RWKEFVRRLGSDHEDIRLELQNGRLREAQYSMLATWRRTRTREATLELLGRVLRDMDL 60
QY 66 DGCVEDL 72
DB 61 LGCLEDI 67

RESULT 14
US-10-041-574-23
; Sequence 23, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-23

Query Match 33.1%; Score 136.5; DB 13; Length 68;
Best Local Similarity 46.3%; Pred. No. 7.7e-09;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps

QY 9 RWKEFVRTIGLREARTEAVEIGR-FRDOQVEMLKRWQ--QQPAGLGAVYAALERMGL 65
DB 1 RWKEFVRRLGSDHEDIRLELQNGRLREAQYSMLATWRRTRTREATLELLGRVLRDMDL 60
QY 66 DGCVEDL 72
DB 61 LGCLEDI 67

RESULT 15

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Search completed: June 27, 2005, 14:53:23
Job time : 164 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2005, 14:32:34 ; Search time 43 Seconds
(without alignments)
138.882 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVRLTLGLR.....ERMGLDGCVEDLRSLRQGP 80

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 307244

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	81.8	65	3	US-09-527-236A-24
2	338	81.8	65	4	US-09-756-854-24
3	155	37.5	78	4	US-08-828-683A-23
4	142	34.4	70	4	US-09-159-277A-6
5	142	34.4	70	4	US-08-844-691A-6
6	136.5	33.1	68	3	US-09-527-236A-23
7	136.5	33.1	68	4	US-09-756-854-23
8	118	28.6	64	3	US-08-894-626-3
9	102.5	24.8	45	2	US-08-219-237B-11
10	83	20.1	67	3	US-09-527-236A-26
11	83	20.1	67	4	US-09-756-854-26
12	73.5	17.8	41	1	US-08-444-005-28
13	70.5	17.1	77	3	US-08-995-159-7
14	70.5	17.1	77	4	US-08-828-683A-27
15	70.5	17.1	77	4	US-09-545-605-7
16	68	16.5	40	1	US-08-444-005-22
17	68	16.5	67	3	US-09-527-236A-25
18	68	16.5	67	4	US-09-756-854-25
19	67	16.2	41	1	US-08-444-005-23
20	67	16.2	51	3	US-08-883-036A-4
21	67	16.2	51	4	US-09-536-201-4
22	67	16.2	51	4	US-09-578-392-4
23	65.5	15.9	41	1	US-08-444-005-29
24	60	14.5	77	4	US-09-069-827A-118
25	59	14.3	68	3	US-08-995-050-1
26	57.5	13.9	45	2	US-08-219-237B-10
27	57.5	13.9	63	3	US-08-894-626-1

28	57.5	13.9	68	3	US-09-527-236A-22	Sequence 22, Appl
29	57.5	13.9	68	4	US-09-756-854-22	Sequence 22, Appl
30	57.5	13.9	70	4	US-09-159-277A-5	Sequence 5, Appl
31	57.5	13.9	70	4	US-08-844-691A-5	Sequence 5, Appl
32	57.5	13.9	77	4	US-08-828-683A-24	Sequence 24, Appl
33	54.5	13.2	63	3	US-08-894-626-2	Sequence 2, Appl
34	54	13.1	25	2	US-08-580-988A-27	Sequence 27, Appl
35	54	13.1	56	3	US-08-894-626-4	Sequence 4, Appl
36	50.5	12.2	74	3	US-09-134-001C-5122	Sequence 5122, Ap
37	50	12.1	37	4	US-09-653-465B-6	Sequence 6, Appl
38	50	12.1	67	3	US-09-527-236A-21	Sequence 21, Appl
39	50	12.1	67	4	US-09-756-854-21	Sequence 21, Appl
40	49	11.9	67	4	US-09-902-540-10142	Sequence 10142, A
41	49	11.9	68	3	US-09-134-001C-3076	Sequence 3076, Ap
42	49	11.9	68	3	US-09-134-001C-3335	Sequence 3335, Ap
43	49	11.9	68	3	US-09-134-001C-3730	Sequence 3730, Ap
44	49	11.9	68	3	US-09-134-001C-3898	Sequence 3898, Ap
45	49	11.9	68	3	US-09-134-001C-4232	Sequence 4232, Ap

ALIGNMENTS

RESULT 1
US-09-527-236A-24
; Sequence 22, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-24

Query Match 81.8%; Score 338; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 6.2e-37; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 0

Qy	9	RWKEFVRLTLGLREAEIAVEVEIGRFRDQYEMLKRWRFQQPAGLGAVYAALERMGLDGC	68
Db	1	RWKEFVRLTLGLREAEIAVEVEIGRFRDQYEMLKRWRFQQPAGLGAVYAALERMGLDGC	60

RESULT 2
US-09-756-854-24
; Sequence 24, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping

```
;
; Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
;
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24

Query Match      81.8%; Score 338; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 6.2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  9 RWKSFVRLGLREAIEAIVEIGRFDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC 68
Db  1 RWKSFVRLGLREAIEAIVEIGRFDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC 60

Qy  69 VEDLR 73
Db  61 VEDLR 65

RESULT 3
US-08-828-683A-23
; Sequence 23, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Li AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
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;
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-828-683A-23

Query Match      37.5%; Score 155; DB 4; Length 78;
Best Local Similarity 46.1%; Pred. No. 7.7e-13;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;

Qy  1 VMDAVPARRWKEFVRTGLREAIEAIVEIGR-FRQQYEMLKRWRQQQP---AGLGAV 56
Db  1 VVENVPPLRWKEFVRLGLSDHEIDRLQLNGRCLREAQYSMLATWRRTPRRATLELL 60

Qy  57 YAALERMGLDGCVEDL 72
Db  61 GRVLRMDMLLGLLEDI 76

RESULT 4
US-09-159-277A-6
; Sequence 6, Application US/09159277A
; Patent No. 6562797
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: O'ROURKE, KAREN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
; TITLE OF INVENTION: FAS-ASSOCIATED APOPTOSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/159,277A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,691
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: US 08/416,379
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442107001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
```

```
;
; TELEFAX: (650)494-0792
; TELEX: 706141 MRNFOERS SFO
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Leu is replaced by Asn for
; OTHER INFORMATION: the point mutant hTNR-1"
US-08-844-691A-6

Query Match 34.4%; Score 142; DB 4; Length 70;
Best Local Similarity 47.1%; Pred No. 3.4e-11;
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

QY 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQQQP---AGLGAVYAALERMG 64
Db 1 RWKEFVRRLGLSDHEIDRLQNGRCLEAQYSMLATWRRTPREATLELLGRVLRDMD 60
QY 65 LDGCVEDL 72
Db 61 LLGCLEDI 68

RESULT 5
US-08-844-691A-6
; Sequence 6, Application US/08844691A
; Patent No. 6747138
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: O'ROURKE, KAREN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
; TITLE OF INVENTION: FAS-ASSOCIATED APOPTOSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,691A
; FILING DATE: 21-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,379
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Koneki, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442107001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)813-5600
; TELEFAX: (650)494-0792
; TELEX: 706141 MRNFOERS SFO
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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;
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Leu is replaced by Asn for
; OTHER INFORMATION: the point mutant hTNR-1"
US-08-844-691A-6

Query Match 34.4%; Score 142; DB 4; Length 70;
Best Local Similarity 47.1%; Pred No. 3.4e-11;
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

QY 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQQQP---AGLGAVYAALERMG 64
Db 1 RWKEFVRRLGLSDHEIDRLQNGRCLEAQYSMLATWRRTPREATLELLGRVLRDMD 60
QY 65 LDGCVEDL 72
Db 61 LLGCLEDI 68

RESULT 6
US-09-527-236A-23
; Sequence 23, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-23

Query Match 33.1%; Score 136.5; DB 3; Length 68;
Best Local Similarity 46.3%; Pred No. 1.7e-10;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQ--QQPAGLGAVYAALERMGL 65
Db 1 RWKEFVRRLGLSDHEIDRLQNGRCLEAQYSMLATWRRTPREATLELLGRVLRDMDL 60
QY 66 DGCVEDL 72
Db 61 LGCLEDI 67

RESULT 7
US-09-756-854-23
; Sequence 23, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
;
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-756-854-23

Query Match 33.1%; Score 136.5; DB 4; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.7e-10;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

Qy 9 RWKEFVRTLGLREAEIEAVEVEIGR-FRDOQYEMLKRWQ--QQPAGLGAVYAALERMGL 65
Db 1 RWKEFVRLGLSDHIDRLQLNGRCLEAQYSMLATWRRRTREATLLGLRVLRMDL 60

Qy 66 DGCVEDL 72
Db 61 LGCLEDI 67

RESULT 8
US-08-894-626-3
; Sequence 3, Application US/08894626
; Patent No. 6355780
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; BOLDIN, Mark P.
; VARFOLOMEV, Eugene E.
; PANCER, Zeev
; METT, Igor
; GONCHAROV, Tanya M.
; WEINWURZEL, Henry
;
; TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08219237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,626
; FILING DATE: 09-Dec-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 112,742
; FILING DATE: 22-FEB-1995
; APPLICATION NUMBER: IL 115,289
; FILING DATE: 13-SEP-1995
; APPLICATION NUMBER: PCT/US96/02326
; FILING DATE: 15-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-894-626-3

Query Match 28.6%; Score 118; DB 3; Length 64;
Best Local Similarity 42.6%; Pred. No. 4.3e-08;
Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;

Qy 10 WKKEFVRTLGLREAEIEAVEVEIGR-FRDOQYEMLKRWQOQPAGLGAVYAALERMG---- 64
Db 1 WKKEFVRLGLSDHIDRLQLNGRCLEAQYSMLATWRRTPRR-----EATLELLGRVLR 56

Qy 65 ---LDGCV 69
Db 57 DHDLGLCL 64

RESULT 9
US-08-219-237B-11
; Sequence 11, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P. O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-11

Query Match 24.8%; Score 102.5; DB 2; Length 45;
Best Local Similarity 51.2%; Pred. No. 2.9e-06;
Matches 21; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

Qy 11 KEFVRTGLREAEIAEVEIGR-FRDOQYEMLKRWQQQP 50
Db 1 KEFVRTGLSDHEIDRLQLNGRCLEAQYSLATWRRTP 41

RESULT 10
US-09-527-236A-26
; Sequence 26, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 26
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-26

Query Match 20.1%; Score 83; DB 3; Length 67;
Best Local Similarity 33.3%; Pred. No. 0.0018;
Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

Qy 10 WKEFVRTGLREAEIAEVEIGRFRDOQYEMLKRW--RQQPAGLGVYAALERMG 64
Db 2 WEPLMRKLGMDNEIKVAKAEAGHRDLYTMLIKWVNTKGRDASVHTLLDALETG 58

RESULT 11
US-09-756-854-26
; Sequence 26, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
```

```
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-756-854-26

Query Match 20.1%; Score 83; DB 4; Length 67;
Best Local Similarity 33.3%; Pred. No. 0.0018;
Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

Qy 10 WKEFVRTGLREAEIAEVEIGRFRDOQYEMLKRW--RQQPAGLGVYAALERMG 64
Db 2 WEPLMRKLGMDNEIKVAKAEAGHRDLYTMLIKWVNTKGRDASVHTLLDALETG 58

RESULT 12
US-08-444-005-28
; Sequence 28, Application US/08444005
; Patent No. 5674734
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Seed, Brian
; APPLICANT: Stanger, Ben Z.
; APPLICANT: Lee, Tae-Ho
; APPLICANT: Kim, Emily
; TITLE OF INVENTION: CELL DEATH PROTEIN
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,005
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,164
; REFERENCE/DOCKET NUMBER: 00383/026001
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Qy 8 R R W K E F V R T L G L R A E A I E A V E I G R - - F R D Q Q Y E M L K R W R Q Q - - - P A G I G A V A Y A A L E R 62

Search completed: June 27, 2005, 14:42:24
Job time : 44 secs

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